



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 99448

TO: Karen A Lacourciere
Location: CM1/11D09/11E12
Art Unit : 1635
Friday, July 25, 2003

Case Serial Number: 08765244

From : Susan Hanley
Location: Biotech-Chem Library
CM1 6B05
Phone: 305-4053

susan.hanley@uspto.gov

Search Notes



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 – Circ. Desk



STIC-Biotech/ChemLib

99448

RECEIVED

JUL 23 2003

(STIC)

From: Lacourciere, Karen
Sent: Tuesday, July 22, 2003 5:29 PM
To: STIC-Biotech/ChemLib
Subject: sequence search request 08/765,244

Please search SEQ ID NO:1 and 22 in the amino acid databases for 08/765,244. Thank-you!

Karen A. Lacourciere Ph.D.

CM1 11D09 GAU 1635
(703) 308-7523

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2003, 21:59:18 ; Search time 36.119 seconds
(without alignments)
180.176 Million cell updates/sec

Title: US-08-765-244-1
Perfect score: 208
Sequence: 1 MSLNRLILLKAALRKAKHTS.....VRNFRYKPVQSQLKPRDLC 41

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Genes19Jun03.*

- 1: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1980.DAT.*
- 2: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1981.DAT.*
- 3: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1982.DAT.*
- 4: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1983.DAT.*
- 5: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1984.DAT.*
- 6: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1985.DAT.*
- 7: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1986.DAT.*
- 8: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1987.DAT.*
- 9: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1988.DAT.*
- 10: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1989.DAT.*
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- 14: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1993.DAT.*
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- 20: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1999.DAT.*
- 21: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2000.DAT.*
- 22: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
- 23: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*
- 24: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	197	94.7	43	17 AAR90584	Rat ornithine tran
2	159	76.4	32	23 ABG30857	Rat ornithine tran
3	108	51.9	32	23 ABG30856	Human ornithine tr
4	108	51.9	258	21 AAB18445	Protein encoded by
5	105	50.5	32	22 AAG64224	OTC peptide fragme
6	92	44.2	32	15 AAR48260	Mitochondrial matr
7	92	44.2	32	20 AAW96358	Mitochondrial matr
8	92	44.2	32	23 ABG92993	Localisation seque
9	92	44.2	32	24 ABP56588	Mitochondrial matr

10	79.5	38.2	31	21 AAB15704	Mitochondrial matr
11	79.5	38.2	31	21 AAB22835	Mitochondrial matr
12	58	27.9	165	20 AAY04933	Mycobacterium spec
13	55.5	26.7	149	22 AAU23468	Novel human enzyme
14	55.5	26.7	761	22 AAB46718	S. cerevisiae DNA
15	54.5	26.2	138	21 AAY75465	Neisseria meningit
16	54.5	26.2	138	21 AAY75466	Neisseria meningit
17	51.5	24.8	280	21 AAG04153	Arabidopsis thalia
18	51.5	24.8	283	21 AAG04152	Arabidopsis thalia
19	51.5	24.8	303	21 AAG26195	Arabidopsis thalia
20	51.5	24.8	303	21 AAG37586	Arabidopsis thalia
21	51.5	24.8	306	21 AAG26194	Arabidopsis thalia
22	51.5	24.8	306	21 AAG37585	Arabidopsis thalia
23	51	24.5	135	6 AAP30637	Salmon pleopionela
24	50.5	24.3	296	22 ABB64170	Drosophila melanog
25	50.5	24.3	755	22 ABB95259	Drosophila melanog
26	50	24.0	136	22 ABB74673	Human protease and
27	50	24.0	193	23 ABB89739	Human polypeptide
28	50	24.0	250	23 ABB99949	Dipeptidyl peptida
29	50	24.0	310	22 ABA47188	Human DPP8 524phe-
30	50	24.0	310	23 ABB08994	Human dipeptidyl p
31	50	24.0	465	22 ABA47189	Human DPP8 319thr-
32	50	24.0	593	20 AAY50124	Human vesicle tran
33	50	24.0	593	20 AAW70702	Human vesicle tran
34	50	24.0	593	22 AAB31567	Amino acid sequenc
35	50	24.0	632	22 AAB93565	Human protein sequ
36	50	24.0	724	23 ABB97362	Novel human protei
37	50	24.0	782	23 ABB97361	Novel human protei
38	50	24.0	866	22 ABB57741	Drosophila melanog
39	50	24.0	882	22 ABA47187	Human DPP8. Homo
40	50	24.0	882	23 AAB24170	Human dipeptidyl p
41	50	24.0	882	23 ABB61591	Human DPPIV relate
42	50	24.0	882	23 AAW74749	Human protease PRT
43	50	24.0	882	23 AAG78415	Amino acid sequenc
44	50	24.0	882	24 ABO07720	Human serine prote
45	49.5	23.8	115	23 ABP02239	Human ORFX protein

ALIGNMENTS

RESULT 1
AAR90584
ID AAR90584 standard; Protein; 43 AA.
AC AAR90584;
XX
XX 25-MAR-2003 (updated)
DT 31-OCT-1996 (first entry)
XX
XX Rat ornithine transcarbamylase signal peptide.
DE
XX promoter; peptide-nucleic acid; cyclised; gene therapy; target;
KW site-directed mutagenesis; introduction; protein transport.
XX
XX Synthetic.
OS
XX
PN DE19520815-A1.
XX
PD 21-DEC-1995.
XX
PF 11-JUN-1995; 95DE-1020815.
XX
PR 16-JUN-1994; 94DE-4421079.
XX
XX (SEIB/) SEIBEL P.
PA
XX Seibel A, Seibel P;
XX
XX WPI; 1996-041226/05.
XX
XX Replicable and transcriptionally active plasmid carrying signal
PT peptide for specific target - useful for site directed mutagenesis

PT and molecular therapy of genetic diseases.

XX Disclosure; Column 11; 24pp; German.

PS

XX Two modified oligonucleotides (introducing PstI and XhoI sites) were used to amplify a region of the human mitochondrial (mt) genome contg. the light strand promoter, mtDNA ori of the heavy strand, CSB's ("conserved sequence blocks") and a regulation site for DNA replication. Behind this fragment (5' direction) a synthetic multiple cloning site was introduced, generating a product with overhang ends. The synthetic region also introduced a bidirectional mt transcription termination sequence. The amplification product, synthetic fragment and pBluescript were ligated and recombinant plasmid 1 (AA12315) was produced. Human mt 16S rRNA (differing from the native RNA only in having a modified nucleotide) was isolated by PCR from chloramphenicol resistant HeLa cells and inserted into plasmid 1 to form plasmid 2 (AA12316). The cloned insert was isolated as a BsaI fragment and cyclised using hairpin loop oligonucleotides, one of which carried the required signal peptide (the present sequence). The cyclised product was purified by treatment with exonuclease III. In a modification, the signal peptide was attached after cyclisation. The new plasmids were able to impart chloramphenicol resistance to otherwise sensitive B lymphocytes and fibroblasts. Similar plasmids without a signal peptide could not do this. The plasmids can be introduced into eukaryotic cells, esp. for site-directed mutagenesis or molecular therapy of genetic diseases, targeting nucleic acid in cells or their organelles via the protein transport route. (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 43 AA;

SQ

Query Match 94.7%; Score 197; DB 17; Length 43;
Best Local Similarity 95.3%; Pred. No. 1.1e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MLSNRIILNKALRKAKHTSMVRNFRYKGPVQS--QLKPRDLC 41
|||||
DB 1 MLSNRIILNKALRKAKHTSMVRNFRYKGPVSQVLKPRDLC 43
|||||

RESULT 2
ABG30857
ID ABG30857 standard; Peptide; 32 AA.
XX
AC ABG30857;
XX
DT 07-OCT-2002 (first entry)
XX
DE Rat ornithine transcarbamylase signal peptide.
DE
XX
KW Rat; signal peptide; ornithine transcarbamylase; MOT;
KW recombinant vector; fusion protein; extranuclear gene.
XX
OS Rattus sp.
XX
PN JP2002176988-A.
XX
PD 25-JUN-2002.
XX
PF 14-DEC-2000; 2000JP-0380975.
XX
PR 14-DEC-2000; 2000JP-0380975.
XX
PA (TANA/) TANAKA M.
PA (GIFU-) ZH GIFUKEN KOKUSAI BIO KENYUJO.
PA (OYOS-) ZH OYO SEIKAGAKU KENKYUSHO.
XX
DR WPI: 2002-569946/61.
DR N-PSDB; ABR88419.
XX
PT A recombinant vector for expressing a fused protein, useful for decomposing an extranuclear gene of a nonhuman organism -
PS Disclosure; Page 3; 15pp; Japanese.

XX The invention relates to a recombinant vector for expressing a fused protein containing a fused gene in which a base sequence defining a transfer signal peptide to small cellular organs having an extranuclear gene is combined with a base sequence defining the amino acid sequence of a restriction enzyme recognising a defined base sequence. The vector is used for decomposing an extranuclear gene of a nonhuman organism. CC The present sequence represents the signal peptide of rat mitochondrial ornithine transcarbamylase (MOT) which may be used in the vector of the invention. CC
XX Sequence 32 AA;
SQ

Query Match 76.4%; Score 159; DB 23; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.6e-18;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSNRIILNKALRKAKHTSMVRNFRYKGPVQ 32
|||||
DB 1 MLSNRIILNKALRKAKHTSMVRNFRYKGPVQ 32
|||||

RESULT 3
ABG30856
ID ABG30856 standard; Peptide; 32 AA.
XX
AC ABG30856;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human ornithine transcarbamylase signal peptide.
DE
XX
KW Human; signal peptide; ornithine transcarbamylase; MOT;
KW recombinant vector; fusion protein; extranuclear gene.
XX
OS Homo sapiens.
XX
PN JP2002176988-A.
XX
PD 25-JUN-2002.
XX
PF 14-DEC-2000; 2000JP-0380975.
XX
PR 14-DEC-2000; 2000JP-0380975.
XX
PA (TANA/) TANAKA M.
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PA (OYOS-) ZH OYO SEIKAGAKU KENKYUSHO.
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DR WPI: 2002-569946/61.
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XX Sequence 32 AA;
SQ

Query Match 51.9%; Score 108; DB 23; Length 32;
Best Local Similarity 68.8%; Pred. No. 1.1e-09;
Matches 22; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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PT and molecular therapy of genetic diseases.

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XX Best Local Similarity 95.3%; Pred. No. 1.1e-23;

XX Matches 41; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MLSNRIILNKAAALRKAHTSMVRNFRYKGPVQ 41

DB 1 MLSNRIILNKAAALRKAHTSMVRNFRYKGPVQ 43

RESULT 2

ABG30857

ID ABG30857 standard; Peptide; 32 AA.

XX

XX ABG30857;

XX

XX 07-OCT-2002 (first entry)

XX Rat ornithine transcarbamylase signal peptide.

DE

XX

XX Rat; signal peptide; ornithine transcarbamylase; MOT;

KW recombinant vector; fusion protein; extranuclear gene.

KW

OS Rattus sp.

XX

XX JP2002176988-A.

XX

XX 25-JUN-2002.

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XX 14-DEC-2000; 2000JP-0380975.

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XX 14-DEC-2000; 2000JP-0380975.

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PA (GIFU-) ZH GIFUKEN KOKUSAI BIO KENYUJO.

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XX

XX WPI: 2002-569946/61.

DR N-PSDB; ABK88419.

XX

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XX A recombinant vector for expressing a fused protein, useful for decompounding an extranuclear gene of a nonhuman organism -

PT Disclosure; Page 3; 15pp; Japanese.

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QY 1 MLSNRIILNKAAALRKAHTSMVRNFRYKGPVQ 32

DB 1 MLSNRIILNKAAALRKAHTSMVRNFRYKGPVQ 32

RESULT 3

ABG30856

ID ABG30856 standard; Peptide; 32 AA.

XX

XX ABG30856;

XX

XX 07-OCT-2002 (first entry)

XX Human ornithine transcarbamylase signal peptide.

DE

XX

XX Human; signal peptide; ornithine transcarbamylase; MOT;

KW recombinant vector; fusion protein; extranuclear gene.

KW

OS Homo sapiens.

XX

XX JP2002176988-A.

XX

XX 25-JUN-2002.

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XX 14-DEC-2000; 2000JP-0380975.

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XX 14-DEC-2000; 2000JP-0380975.

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Query Match 51.9%; Score 108; DB 23; Length 32;

XX Best Local Similarity 68.8%; Pred. No. 1.1e-09;

XX Matches 22; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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QY 1 MLSNRIILNKAAALRKAHTSMVRNFRYKGPVQ 32

DB 1 MLSNRIILNKAAALRKAHTSMVRNFRYKGPVQ 32

RESULT 3

ABG30856

ID ABG30856 standard; Peptide; 32 AA.

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XX ABG30856;

XX

XX 07-OCT-2002 (first entry)

XX Human ornithine transcarbamylase signal peptide.

DE

XX

XX Human; signal peptide; ornithine transcarbamylase; MOT;

KW recombinant vector; fusion protein; extranuclear gene.

KW

OS Homo sapiens.

XX

XX JP2002176988-A.

XX

The specification describes a method for functionally complementing one or more defects, mutations, or deletions in a mitochondrial genome of a cell having a nuclear genome. The method is used for treating a disease or disorder that arises from deletion of the protein-encoding genes of the mitochondrial genome. Alternatively, the method is used for treating a disease or disorder that arises from one or more defects, deletions or mutations in mitochondrial genes encoding ribosomes or tRNA for transcription and translation in the mitochondria. The diseases or disorders that can be ameliorated are the mitochondrial encephalomyopathy with lactic acidosis and stroke-like episodes, Leber hereditary optic neuropathy, myoclonic epilepsy with ragged-red fibers, neurogenic muscular weakness, ataxia, retinitis pigmentosa, Kearns-Sayre syndrome; Leigh syndrome, Pearson Marrow pancreas syndrome, aminoglycoside-associated deafness, diabetes with deafness, leukodystrophy with hypotonia, autism with seizures, sudden infant death syndrome with hypoglycaemia, leukaemia with maternally inherited thrombocytopenia, migraines (associated with hearing loss, strokes, or diabetes), early hearing loss, refractory infantile reflux with carnitine deficiency, multiple sclerosis with seizures, blindness with optic atrophy and dystonia, renal tubular acidosis with elevated lactic acid and hypotonia, nonvalvular hypertrophic cardiomyopathy before age 50 and chronic pancreatitis with stroke-like episodes. The present sequence is encoded by plasmid pUOATP2. Stroke-like episodes. The present sequence is encoded

```

XX DE Mitochondrial matrix retention signal.
XX DE
XX KW Single chain antibody; sFv; heavy chain; light chain;
XX KW variable domain; hydrophilic linker; antibodies; targeting;
XX KW subcellular localisation signal; mitochondrial matrix;
XX KW retention signal.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Misc-difference 7 /note= "not defined"
XX FT Misc-difference 8 /note= "not defined"
XX FT Misc-difference 32 /note= "not defined"
XX PN WO9402610-A1.
XX PD 03-FEB-1994.
XX PF 16-JUL-1993; 93WO-US06735.
XX PR 17-JUL-1992; 92US-0916939.
XX PR 17-MAR-1993; 93US-0045274.
XX PA (DAND ) DANA FARBER CANCER INST INC.
XX PI Haseltine WA, Marasco WA;
XX DR WPI; 1994-048868/06.
XX PT Intracellular binding of antigens - by using antibody targeting
XX PT with vector system, for e.g. tumour suppression
XX PS Disclosure; Page 103; 155pp; English.
XX CC New vector systems comprise a sequence adapted for intracellular
XX CC delivery and expression contg. a promoter operably linked to an
XX CC antibody gene encoding an antibody which binds to a specific target
XX CC antigen. The antibody is esp. a single chain antibody in which the
XX CC heavy and light chain variable regions are joined via a hydrophilic
XX CC linker peptide. Localisation sequences are pref. included in the
XX CC constructs. The sequence AAR48260 is a mitochondrial matrix retention
XX CC signal.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 32 AA;
Query Match 44.2%; Score 92; DB 15; Length 32;
Best Local Similarity 61.3%; Pred. No. 3.9e-07;
Matches 19; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
QY 1 MLSNLRILLNKAALRKAHTSMVRNFRYKGPV 31
DB 1 MLFNLRXXLLNNAAFRRGHNFVRNFRCGQPL 31
RESULT 7
ID AAW96358
XX AAW96358 standard; Peptide; 32 AA.
XX AC AAW96358;
XX DT 19-JUL-1999 (first entry)
XX DE Mitochondrial matrix localisation signal peptide.
XX KW Antibody; immune response; modulation; MHC; IRM; receptor;
XX KW intrabody; major histocompatibility complex; graft rejection;
XX KW immunomodulatory response molecule; regulation; transplantation;
XX KW retention signal; localisation signal; golgi apparatus; ER;

```

```

KW endoplasmic reticulum.
XX Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 7 /note= "Any amino acid"
XX FT Misc-difference 8 /note= "Any amino acid"
XX FT Misc-difference 32 /note= "Any amino acid"
XX PN WO9914353-A2.
XX PD 25-MAR-1999.
XX PF 18-SEP-1998; 98WO-US19563.
XX PR 19-SEP-1997; 97US-0059339.
XX PA (DAND ) DANA FARBER CANCER INST INC.
XX PI Marasco W, Mhashikar A;
XX DR WPI; 1999-229546/19.
XX PT Altering the regulation of the immune system
XX PS Disclosure; Page 28; 56pp; English.
XX CC Intracellular binding to a desired target by an intracellularly
XX CC expressed antibody (i.e. an intrabody) can be used to knock out
XX CC multiple locuses of immunomodulatory receptor molecules (IRMs),
XX CC so that the expression of multiple major histocompatibility (MHC)
XX CC molecules is blocked. This selective targeting of IRMs, their
XX CC pathways or components, can be used to selectively regulate the
XX CC immune system by controlling expression of these molecules and
XX CC preventing an undesired immune response in a cell. Any component
XX CC of the MHC pathway or the MHC assembly line or antigen presentation
XX CC can be targeted. Intrabodies can be used to knock out the immune
XX CC response in a particular tissue or portion of the body to prepare
XX CC it for cell or tissue transplantation. Alternatively, an organ for
XX CC transplantation can be perfused with the intrabody ex vivo. The
XX CC intrabodies can comprise whole antibodies, heavy chains, Fab'
XX CC fragments, single-chain antibodies and diabodies. The intrabodies
XX CC also comprise an intracellular localisation signal to facilitate
XX CC interception of expressed proteins. For example, if the target was
XX CC a cell surface receptor, the antibody would comprise a leader
XX CC sequence and an endoplasmic reticulum (ER) or Golgi apparatus
XX CC retention signal. This peptide is a localisation sequence for the
XX CC mitochondrial matrix. For other localisation sequences see
XX CC AAW96345-W96377.
XX SQ Sequence 32 AA;
Query Match 44.2%; Score 92; DB 20; Length 32;
Best Local Similarity 61.3%; Pred. No. 3.9e-07;
Matches 19; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
QY 1 MLSNLRILLNKAALRKAHTSMVRNFRYKGPV 31
DB 1 MLFNLRXXLLNNAAFRRGHNFVRNFRCGQPL 31
RESULT 8
ID ABG92993
XX ABG92993 standard; Peptide; 32 AA.
XX AC ABG92993;
XX DT 20-NOV-2002 (first entry)
XX DE Localisation sequence to direct antibodies to the mitochondria.

```

Regulator; transcription; cell death; phenotype; molecular scaffold; gene therapy; cancer; cardiovascular disease; arrhythmia; heart failure; ischemia; obesity; neurodegenerative disease; Alzheimer's disease; bone pathology; dermatologic disease; psoriasis; infection; AIDS; acquired immunodeficiency syndrome; cosmetic; wound healing; antibiotic transport; drug toxicity; drug resistance; immunobiology; inflammation; allergic response; human immunodeficiency virus.

Unidentified.

WO200262822-A2.

15-AUG-2002.

04-FEB-2002; 2002WO-US02814.

02-FEB-2001; 2001US-265899P.

05-FEB-2001; 2001US-265880P.

27-FEB-2001; 2001US-371423P.

23-JAN-2001; 2001US-263226P.

28-MAR-2000; 2000US-192586P.

22-SEP-1997; 97US-935377P.

(UYRP) UNIV ROCHESTER.

Zauderer M, Smith ES;

WPI; 2002-643398/59.

Identifying regulator polypeptides which influence target transcriptional regulatory regions, useful for treating cancer, comprises introducing host cells expressing the polypeptide into a library of polynucleotides.

Disclosure; Page 37; 224pp; English.

The invention discloses a method for identifying polynucleotides encoding a regulator polypeptide, whose expression induces activation of a target transcriptional regulatory region in a host cell. The method comprises providing a population of eukaryotic host cells capable of expressing the polypeptide, introducing into the host cell a library of polynucleotides encoding the polypeptides, permitting expression of the polypeptides and then recovering them from the host cells. The target transcriptional regulatory region is operably associated with a polynucleotide encoding a gene product, the expression of which results in host cell death or cause the host cells to exhibit a pre-determined modified phenotype and where the gene product is expressed upon activation of target transcriptional regulatory region. Each candidate regulator polypeptide comprises a candidate peptide and a molecular scaffold fused to the peptide so that the peptide is displayed on the surface of the candidate regulator polypeptide. The methods are useful in selecting and/or screening regulator molecules, such as polypeptides, which directly or indirectly induce or suppress the transcriptional activation of a target transcriptional regulatory region in a eukaryotic host cell. These regulator molecules may be used (e.g. in gene therapy) for preventing or treating cancers (e.g. breast or ovarian cancer), cardiovascular diseases (e.g. arrhythmia, heart failure, ischemia), obesity, neurodegenerative diseases (e.g. Alzheimer's disease), bone pathologies, dermatologic diseases (e.g. psoriasis), infections (e.g. viral, bacterial), acquired immunodeficiency syndrome (AIDS), in cosmetic applications and in wound healing. The method is also useful in screening regulator molecules that block antibiotic transport mechanisms, in drug toxicities and drug resistance applications and in improving the performance of existing or developmental drugs. It may also be used in immunobiology, inflammation, allergic response and in biotechnology applications. The sequences presented in ABG92946-ABG93029 are examples of regulator polypeptides.

Sequence 32 AA;

Query Watch 44.2%; Score 92; DB 23; Length 32;

Best Local Similarity 61.3%; Pred. No. 3.9e-07;

Matches 19; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSLNRLILNKAALRKAHTSMVRNRYGKPV 31

DB 1 MLFNLRXXLNNAAPRHGHNVNFRGQQL 31

RESULT 9

ABP56588

ID ABP56588 standard; Peptide; 32 AA.

XX

AC ABP56588;

XX

DT 24-MAR-2003 (first entry)

XX

DE Mitochondrial matrix targeting peptide SEQ ID NO:54.

XX

KW Identification; intrabody; eukaryotic cell; immunoglobulin; selection;

KW cardiovascular; diminished arrhythmia potential; cardiomyocyte; stroke;

KW enhanced contractile property; heart failure; arrhythmia; embolic;

KW sarcolemmal calcium cycling; artery; arteriole; angina; atherosclerosis;

XX LDL metabolism; HDL metabolism; skin biology; keloid formation.

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Misc-difference 7 /note= "any amino acid"

FT Misc-difference 8 /note= "any amino acid"

FT Misc-difference 32 /note= "any amino acid"

FT Misc-difference 32 /note= "any amino acid"

PN WO200286096-A2.

XX

PD 31-OCT-2002.

XX

PF 23-JAN-2002; 2002WO-US01677.

XX

PR 23-JAN-2001; 2001US-263225P.

PR 24-JAN-2001; 2001US-263220P.

PR 27-FEB-2001; 2001US-271422P.

PR 15-JUN-2001; 2001US-298095P.

XX

PA (UYRP) UNIV ROCHESTER MEDICAL CENT.

XX

PI Zauderer M, Wei C, Smith ES;

XX

DR WPI; 2003-103408/09.

XX

PT Selecting polynucleotides encoding an intracellular immunoglobulin

PT which induces a modified phenotype in a eukaryotic host cell, by

PT introducing library of polynucleotides encoding immunoglobulin subunit

PT polypeptides -

XX

PS Disclosure; Page 44; 257pp; English.

XX

CC The present invention describes a method for selecting polynucleotides

CC (PNS) encoding an intracellular immunoglobulin molecule or its fragment

CC whose expression induces a modified phenotype in a eukaryotic host cell

CC (I). The method comprises introducing into (I) a first and second library

CC of PNS encoding, through operable association with a transcriptional

CC control region, first and second intracellular immunoglobulin subunit

CC polypeptides, respectively. The method is useful for selecting

CC polynucleotides which encode an intracellular immunoglobulin molecule, or

CC fragment. The method is useful e.g. for identifying polynucleotides which

CC singly or collectively encode intracellular immunoglobulin molecules, or

CC which sensitize host cells to killing by an agent. The method may also be

CC used in cardiovascular applications; for screening for diminished

CC arrhythmia potential in cardiomyocytes and for enhanced contractile

CC properties of cardiomyocytes and diminish heart failure potential; for

CC identifying intracellular immunoglobulin molecules that will regulate

CC intracellular and sarcolemmal calcium cycling in cardiomyocytes to

CC prevent arrhythmias or that will diminish embolic phenomena in arteries

Query Match 27.9%; Score 58; DB 20; Length 165;
Best Local Similarity 39.4%; Pred. No. 0.73;

PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231142.
PR 08-SEP-2000; 2000US-0231143.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 13-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.

PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI: 2001-465565/50.
DR N-PSDB: AAS41338.
XX
PT Novel polypeptides and polynucleotides useful for diagnosing,
PT preventing, treating neural, immune system, muscular, reproductive,
PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous
PT diseases
XX
PS Claim 11; SEQ ID NO 1464; 1180pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders
CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
CC blood-related disorders (e.g. haemophilia), reproductive disorders
CC (e.g. infertility) and infectious disorders (e.g. influenza). The
CC polynucleotides of the invention can also be used in gene therapy.
CC AAU22915-AAU23814 represent the novel human enzyme polypeptides of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 149 AA;

Query Match 26.7%; Score 55.5; DB 22; Length 149;
Best Local Similarity 35.3%; Pred. NO. 1.6;
Matches 18; Conservative 6; Mismatches 10; Indels 17; Gaps 3;

QY 5 LRLLNK-----AALRKAHTSMYRFRYG-----KPVQSQL---KPR 38
||: || | ||| :||: ||
Db 52 LRMTLQKESAMIAIRSRKPHATMIRNAKYSGLHAGWSLWPVESALQSHQPR 102
||: || | ||| :||: ||

RESULT 14
AAB46718
ID AAB46718 standard; Protein; 761 AA.
XX
AC AAB46718;

```

XX 12-APR-2001 (first entry)
XX S. cerevisiae DNA polymerase protein fragment SEQ ID NO 27.
DE Genome; thermophilic enzyme; washing powder; bleaching.
XX Saccharomyces cerevisiae.
XX WO200075335-A2.
XX 14-DEC-2000.
XX 02-JUN-2000; 2000WO-IB00893.
XX 02-JUN-1999; 99US-0137120.
XX (DECO-) DECODE GENETICS EHF.
XX Hjorleifsdottir S, Hreggvidsson GO, Fridjonsson OH, Aevartsson A;
PI Kristjansson JK;
XX WPI; 2001-061727/07.
XX Isolated nucleic acid from bacteriophage RM 378 encoding enzymes useful
PT in recombinant DNA technology -
XX Disclosure; Figure 3A-P; 42pp; English.
XX This invention describes a novel isolated nucleic molecule (I) comprising
CC the genome of bacteriophage RM 378. The invention also describes (1) an
CC isolated nucleic acid which encodes a polypeptide obtainable from
CC bacteriophage RM 378, or its active derivative or fragment; (2) an
CC isolated bacteriophage RM 378 (III); (3) a DNA construct (III) comprising
CC operatively linked to a regulatory sequence; (4) a host cell comprising
CC (III); and (5) an isolated polypeptide (IV) obtainable from (III), its
CC active derivative or fragment. Bacteriophage RM 378 is useful for
CC producing thermophilic enzymes useful in DNA research and commercial
CC settings (e.g. proteases and lipases used in washing powder, hydrolytic
CC enzymes used in bleaching). The isolated nucleic acid molecules and
CC vectors are useful in the manufacture of encoded polypeptide, as probes
CC for isolating homologous sequences (e.g. from other bacteriophage
CC species), as well as for detecting the presence of the bacteriophage in
CC a culture of host cells. The polypeptides can be used as a molecular
CC weight marker on SDS-PAGE gels or on molecular sieve gel filtration
CC columns. Because the host organism of the RM378 bacteriophage is a
CC thermophile, the enzymes and proteins of the RM378 bacteriophage are
CC significantly more thermostable than those of other (e.g. mesophilic)
CC bacteriophages, such as the T4 bacteriophage of Escherichia coli. The
CC enhanced stability of the enzymes and proteins of RM378 bacteriophage
CC allows their use under temperature conditions which would be prohibitive
CC for other enzymes, thus increasing the range of conditions which can be
CC employed not only in DNA research but also in commercial settings.
XX
XX Sequence 761 AA;
Query Match 26.7%; Score 55.5; DB 22; Length 761;
Best Local Similarity 29.4%; Pred. No. 12;
Matches 15; Conservative 4; Mismatches 21; Indels 11; Gaps 1;
QY 2 LSNRLILL-----NKAALRAKHTSMVRNFRYKPVQSQLKPRDLC 41
Db 62 MNPRLCLSLSIOTLMNPKENKQEIYVITLSAFNISLDSQIPENIKPDDLC 112
RESULT 15
AAAY75465
ID AAY75465 standard; Protein; 138 AA.
XX AAY75465;
XX
XX 21-MAR-2000 (first entry)
XX

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```

DE Neisseria meningitidis ORF 715 protein sequence SEQ ID NO:2404.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KW antibacterial; gene therapy.
XX
XX Neisseria meningitidis.
OS
XX WO9957280-A2.
XX 11-NOV-1999.
XX 30-APR-1999; 99WO-US09346.
XX 01-MAY-1998; 98US-0083758.
XX 31-JUL-1998; 98US-0094869.
XX 02-SEP-1998; 98US-0098994.
XX 02-SEP-1998; 98US-0099062.
XX 09-OCT-1998; 98US-0103749.
XX 09-OCT-1998; 98US-0103794.
XX 09-OCT-1998; 98US-0103796.
XX 25-FEB-1999; 99US-0121528.
XX (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
XX WPI; 2000-062150/05.
XX N-PSDB; AAZ54227.
XX
XX Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics -
XX
XX Claim 2; Page 1154; 1453pp; English.
XX
XX AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC and polypeptides AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
CC PCR primers used in the exemplification of the present inventions. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
XX Sequence 138 AA;
Query Match 26.2%; Score 54.5; DB 21; Length 138;
Best Local Similarity 42.9%; Pred. No. 2.1;
Matches 15; Conservative 4; Mismatches 15; Indels 1; Gaps 1;
QY 6 RILLKALRAKHAHTSMVRNFRY-GKPVQSQLKPRD 39
Db 26 RYLLMRLSETMHTAVKLNFRYAGRPKWVGLKYRD 60
Search completed: July 24, 2003, 22:04:07
Job time : 38.119 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 24, 2003, 22:02:54 ; Search time 20.0119 Seconds

(without alignments)
86.686 Million cell updates/sec

Title: US-08-765-244-1

Perfect score: 208

Sequence: 1 MSLNRLILNKAALRKHTS.....VRNPRYKGPVQSOLKPRDLC 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued patents:AA:*

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3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	44.2	32	2	US-08-373-190-29
2	92	44.2	32	2	US-08-438-190A-29
3	92	44.2	32	3	US-08-350-215-29
4	92	44.2	32	3	US-09-287-145A-29
5	92	44.2	32	4	US-09-556-111-29
6	55.5	26.7	761	4	US-09-585-858-27
7	52	25.0	457	4	US-09-252-991A-32812
8	51.5	24.8	208	4	US-09-107-532A-5399
9	50	24.0	310	4	US-09-794-236-4
10	50	24.0	593	2	US-08-900-927-1
11	50	24.0	593	3	US-09-191-279-1
12	50	24.0	593	3	US-09-334-476-1
13	49	23.6	547	4	US-09-252-991A-25705
14	48.5	23.3	274	4	US-09-252-991A-29653
15	48	23.1	39	1	US-08-428-488-13
16	48	23.1	89	4	US-09-732-210-98
17	48	23.1	567	3	US-09-188-811-2
18	47	22.6	20	5	PCT-US95-07543-5
19	47	22.6	91	4	US-09-732-210-195
20	47	22.6	481	4	US-09-130-491-8
21	47	22.6	735	3	US-08-539-205A-2
22	47	22.6	735	4	US-09-392-163A-2
23	47	22.6	905	4	US-09-369-364A-9
24	47	22.6	1050	4	US-09-428-711A-16
25	47	22.6	2539	3	US-09-413-814-42
26	46	22.1	78	2	US-08-327-362-3
27	46	22.1	78	3	US-09-158-565-3

28	45.5	21.9	399	4	US-09-328-352-7632	Sequence 7632, Ap
29	45.5	21.9	548	3	US-08-903-139B-9	Sequence 9, Appl
30	45.5	21.9	548	3	US-08-903-139B-28	Sequence 28, Appl
31	45	21.6	141	4	US-09-428-711A-4	Sequence 4, Appl
32	45	21.6	218	4	US-09-252-991A-18053	Sequence 18053, A
33	45	21.6	375	4	US-09-428-711A-2	Sequence 2, Appl
34	45	21.6	582	4	US-09-107-532A-5110	Sequence 5110, Ap
35	45	21.6	609	4	US-07-846-181-5	Sequence 5, Appl
36	45	21.6	730	1	US-07-845-989-5	Sequence 5, Appl
37	45	21.6	730	1	US-09-252-991A-19085	Sequence 19085, A
38	45	21.6	795	4	US-09-428-711A-14	Sequence 14, Appl
39	45	21.6	1051	4	US-09-914-259-68	Sequence 68, Appl
40	45	21.6	1139	4	US-09-046-479-4	Sequence 4, Appl
41	44.5	21.4	119	3	US-08-822-897C-4	Sequence 4, Appl
42	44.5	21.4	119	4	US-09-608-810A-5	Sequence 5, Appl
43	44.5	21.4	119	4	US-09-252-991A-25726	Sequence 25726, A
44	44.5	21.4	418	4	US-09-457-708-2	Sequence 2, Appl
45	44.5	21.4	1164	4		

ALIGNMENTS

RESULT 1

US-08-373-190-29
; Sequence 29, Application US/08373190
; Patent No. 5851829
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,190
; FILING DATE: 17-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06735
; FILING DATE: 16-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41956-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: STRE UR 2002
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-373-190-29

Query Match

44.2%; Score 92; DB 2; Length 32;

```
0: Gaps 0;
```

STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS

ADDRESSEE: CUSHMAN
STREET. 130 WATER STREET
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
CORRESPONDENCE ADDRESS:

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arianello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5399:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc.feature
LOCATION: (B) LOCATION 1...208
SEQUENCE DESCRIPTION: SEQ ID NO: 5399:
US-09-107-532A-5399
Query Match 24.8%; Score 51.5; DB 4; Length 208;
Best Local Similarity 44.4%; Pred. No. 2.9;
Matches 12; Conservative 3; Mismatches 3; Indels 9; Gaps 1;
QY 10 NKAALRKHAHTSMVRNFRYKPVQSLK 36
Db 59 NKA-----QNFYKPKPTPELE 76
RESULT 9
US-09-794-236-4
Sequence 4, Application US/09794236
Patent No. 6337069
GENERAL INFORMATION:
APPLICANT: Grouzmann, Eric
APPLICANT: Lacroix, Jean-Silvain
APPLICANT: Monod, Michel
TITLE OF INVENTION: Method of Treating Rhinitis and Sinusitis
FILE REFERENCE: 81985/276823
CURRENT APPLICATION NUMBER: US/09/794,236
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 310
TYPE: PRT

us-08-765-244-1-rai
GENERAL INFORMATION:
ORGANISM: Homo sapiens
US-09-794-236-4
Query Match 24.0%; Score 50; DB 4; Length 310;
Best Local Similarity 44.0%; Pred. No. 8.2;
Matches 11; Conservative 6; Mismatches 6; Indels 2; Gaps 1;
QY 17 AHTSMVRNF--RYGKPVQSQLKPRD 39
Db 251 AHTSILSLVLRAGKPYDLQIYPQE 275
RESULT 10
US-08-900-927-1
Sequence 1, Application US/08900927
Patent No. 5840537
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NEW VESICLE TRANSPORT PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,927
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0350 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MMLR20T01
CLONE: 475485
US-08-900-927-1
Query Match 24.0%; Score 50; DB 2; Length 593;
Best Local Similarity 31.1%; Pred. No. 18;
Matches 14; Conservative 9; Mismatches 12; Indels 10; Gaps 2;
QY 4 NLRILNKAALRKHAHTSMVRNFRY-----GKPVQSQLKPRD 39
Db 421 NLAKLIQHANY-QAHSLLRNLEQLGTVNPGSGTSSRLPRE 464
RESULT 11
US-09-191-279-1
Sequence 1, Application US/09191279
Patent No. 5981192
GENERAL INFORMATION:
APPLICANT: Bandman, Olga


```

Query Match      23.1%: Score 48; DB 1: Length 39;
Best Local Similarity 50.0%: Pred. No. 1.4;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      22 VNFYRGKPVQSQKLP 37
      : : : : : : : : : :
Db      4 MEHFYRGKPVGKKRRP 19

Search completed: July 24, 2003, 22:08:52
Job time : 21.0119 secs

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1:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2003, 22:02:24 ; Search time 13.6667 Seconds
(without alignments)
288.506 Million cell updates/sec

Title: US-08-765-244-1
Perfect score: 208
Sequence: 1 MSLNRLINKAALRAHTS.....VRNFRYKGPVQSOLKPRDLIC 41

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-76: *
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	179	86.1	354	1 OWRT	ornithine carbamoy
2	144	69.2	354	1 OWMS	ornithine carbamoy
3	125	60.1	354	1 OWHU	ornithine carbamoy
4	112	53.8	41	1 T52779	ornithine transcar
5	57	27.4	350	2 A48421	ornithine transcar
6	57	27.4	351	2 F90403	GTP binding conser
7	56	26.9	1286	2 B71413	hypothetical prote
8	55.5	26.7	1468	2 S58250	DNA-directed DNA p
9	54.5	26.2	138	2 F81900	hypothetical prote
10	53.5	25.7	260	2 G70233	hypothetical prote
11	53.5	25.7	383	2 B83922	short-chain-specif
12	53	25.5	435	2 S31280	cyclin B5 - yeast
13	52.5	25.2	185	2 B81708	translation elonga
14	51.5	24.8	306	2 T52305	En/Spm-like transp
15	51.5	24.8	314	2 F75504	probable pilin, ty
16	51	24.5	240	2 B45359	proopiomelanocorti
17	51	24.5	258	1 CTONEPK	corticotropin / li
18	51	24.5	506	2 T50211	WD-repeat protein
19	51	24.5	1779	2 T23130	hypothetical prote
20	49.5	23.8	181	2 T32637	hypothetical prote
21	49.5	23.8	425	2 I40646	sensor-like protei
22	49	23.6	178	2 F91180	hypothetical prote
23	49	23.6	178	2 H86026	hypothetical prote
24	49	23.6	276	2 AD3351	spoU family of rRN
25	49	23.6	300	2 T32702	hypothetical prote
26	49	23.6	320	2 AB0194	pseudouridylylate sy
27	49	23.6	353	2 T25678	hypothetical prote
28	49	23.6	355	1 B95518	GTP-binding protei
29	49	23.6	531	1 NNEC2	anthranilate synth

RESULT 1

OWRT

ornithine carbamoyltransferase (EC 2.1.1.3) precursor - rat
N;Alternate names: citrulline phosphorylase; ornithine transcarbamylase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1986 #sequence, revision 28-Feb-1986 #text, change 11-Jun-1999
C;Accession: A00563; A28042; A23090; S02466; I52976; I67609; I53457
R;Takiguchi, M.; Miura, S.; Mori, M.; Tatibana, M.; Nagata, S.; Kaziro, Y.
Proc. Natl. Acad. Sci. U.S.A. 81, 7412-7416, 1984
A;Title: Molecular cloning and nucleotide sequence of cDNA for rat ornithine carbamoyltransferase
A;Reference number: A00563; MUID:85063800; PMID:6095294
A;Accession: A00563
A;Molecule type: mRNA
A;Residues: 1-354 <TAKI>
A;Cross-references: GB:K03040; NID:g205873; PIDN:AAA1768.1; PID:g205874
R;Takiguchi, M.; Murakami, T.; Miura, S.; Mori, M.
Proc. Natl. Acad. Sci. U.S.A. 84, 6136-6140, 1987
A;Title: Structure of the rat ornithine carbamoyltransferase gene, a large, X chromos
A;Reference number: A28042; MUID:87317609; PMID:3476935
A;Accession: A28042
A;Molecule type: DNA
A;Residues: 1-354 <TAK2>
A;Cross-references: GB:M16933; GB:J02957; NID:g205884; PIDN:AAA1769.1; PID:g205886
R;Kraus, J.P.; Hodges, P.E.; Williamson, C.L.; Horwich, A.L.; Kalousek, F.; Williams, Nucleic Acids Res. 13, 943-952, 1985
A;Title: A cDNA clone for the precursor of rat mitochondrial ornithine transcarbamyla
A;Reference number: A23090; MUID:85215524; PMID:3839075
A;Accession: A23090
A;Molecule type: mRNA
A;Residues: 1-38, P', 40-240, S', 242-354 <KRA>
A;Cross-references: GB:X01976
R;Aoki, Y.; Sunaga, H.; Suzuki, K.T.
Biochem. J. 250, 735-742, 1988
A;Title: A cadmium-binding protein in rat liver identified as ornithine carbamoyltran
A;Reference number: S02466; MUID:88268748; PMID:3390141
A;Accession: S02466
A;Molecule type: protein
A;Residues: 33-56; 293-302; 307-317; 322-329 <AOK>
R;McIntyre, P.; Graf, L.; Mercer, J.F.B.; Wake, S.A.; Hudson, P.J.; Hoogenraad, N.
DNA 4, 147-156, 1985
A;Title: The primary structure of the imported mitochondrial protein, ornithine trans
A;Reference number: I52976; MUID:85203360; PMID:3838931
A;Accession: I52976
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>
A;Cross-references: GB:M11266; NID:g205871; PIDN:AAA1767.1; PID:g205872
R;McIntyre, P.; Graf, L.; Mercer, J.; Peterson, G.; Hudson, P.J.; Hoogenraad, N.
FEBS Lett. 177, 41-46, 1984
A;Title: A highly basic N-terminal extension of the mitochondrial matrix enzyme ornit
A;Reference number: I53457; MUID:85051832; PMID:6548714
A;Accession: I67609

ALIGNMENTS

anthranilate synth
hypothetical prote
anthranilate synth
probable sulfatase
invasin - Versinia
Div protein [impor
cation-transportin
protein-tyrosine k
ribosomal protein
probable proteasom
proteasome endopep
hypothetical prote
hypothetical prote
subtilisin-like pr
hypothetical prote
cytochrome-c oxida

30 49 23.6 531 2 C90858
31 49 23.6 531 2 E85761
32 49 23.6 531 2 AE0653
33 49 23.6 538 2 F83354
34 49 23.6 986 1 A29646
35 48.5 23.3 333 2 A10802
36 48.5 23.3 945 2 S77052
37 48.5 23.3 1114 1 S05582
38 48 23.1 89 2 T43306
39 48 23.1 260 2 A71033
40 48 23.1 260 2 B75181
41 48 23.1 362 2 B87613
42 48 23.1 362 2 S76749
43 48 23.1 765 2 T04186
44 48 23.1 893 2 T29621
45 47.5 22.8 260 2 T11798

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-102 <RE2>
A:Cross-references: EMBL:X01178; NID:g56802; PIDN:CAA25618.1; PID:g56803
A:Accession: I53457
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-43,'N',45-99,'R',101-102 <R3>
A:Cross-references: GB:X03041; NID:g205889; PIDN:AAA1171.1; PID:g205890
C:Genetics:
A:Introns: 26/2; 72/3; 100/1; 129/2; 180/3; 221/3; 239/3; 289/3; 335/3
C:Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
C:Keywords: arginine biosynthesis; homotrimer; mitochondrion; transferase; urea cycle
F:1-32/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:33-354/Product: ornithine carbamoyltransferase #status predicted <WAT>
F:40-342/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>

Query Match 86.18; Score 179; DB 1; Length 354;
Best Local Similarity 92.98; Pred. No. 1.0e-17;
Matches 39; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 MLSNLRLLNKAALRAKTSWNRNFRYKPKVQS--QLKPRDL 40
|||||
DB 1 MLSNLRLLNKAALRAKTSWNRNFRYKPKVQSQQLKGRDL 42
|||||

RESULT 2
OWNS
N:Alternate names: citrulline phosphorylase; ornithine transcarbamylase
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1993 #sequence,revision 13-Mar-1997 #text_change 11-Jun-1999
C:Accession: A43609; S03407; I55252
R:Veres, G.; Gibbs, R.A.; Scherer, S.E.; Caskey, C.T.
Science 237, 415-417, 1987
A:Title: The molecular basis of the sparse fur mouse mutation.
A:Reference number: A43609; MUID:87263407; PMID:3603027
A:Accession: A43609
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-354 <VER>
A:Cross-references: GB:M17030; NID:g200162; PIDN:AAA39865.1; PID:g200163
R:Scherer, S.E.; Veres, G.; Caskey, C.T.
Nucleic Acids Res. 16, 1593-1601, 1988
A:Title: The genetic structure of mouse ornithine transcarbamylase.
A:Reference number: S03407; MUID:88157717; PMID:2831503
A:Accession: S03407
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-194,'R',196-335 <SCH>
A:Cross-references: EMBL:X07092
R:Veres, G.; Craigien, W.J.; Caskey, C.T.
J. Biol. Chem. 261, 7588-7591, 1986
A:Title: The 5' flanking region of the ornithine transcarbamylase gene contains DNA sequence information for the 5' noncoding region.
A:Reference number: I55252; MUID:86224037; PMID:3011788
A:Accession: I55252
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19,'LLWPDIF', <RES>
A:Cross-references: GB:M12716; NID:g200160; PIDN:AAA39864.1; PID:g554248
A:Note: The end of this sequence is near the boundary of the cloned region and may be an artifact.
C:Genetics:
A:Gene: OTC
A:Map position: X
A:Introns: 26/2; 72/3; 100/1; 129/2; 180/3; 221/3; 239/3; 289/3
C:Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
C:Keywords: mitochondrion; transferase; urea cycle
F:1-32/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:33-335/Product: ornithine carbamoyltransferase #status predicted <WAT>
F:40-342/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>

Query Match 69.2%; Score 144; DB 1; Length 354;
Best Local Similarity 78.6%; Pred. No. 1.5e-12;

e synthesis of UMP.

C:Comment: The active enzyme catalyzes the condensation of carbamoyl phosphate and ornithine to form citrulline.

C:Genetics: 152779

A:Gene: GDB:OTC

A:Cross-references: GDB:119468; OMIM:311250

A:Map position: XP21.1-Xp21.1

C:Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase

C:Keywords: arginine biosynthesis; homotrimer; mitochondrion; transferase; urea cycle

F:1-32/Domain: transit peptide (mitochondrion) #status predicted <TNP>

F:33-354/Product: ornithine carbamoyltransferase #status predicted <MAT>

F:40-342/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>

Query Match 60.1%; Score 125; DB 1; Length 354;

Best Local Similarity 66.7%; Pred. No. 7.3e-10;

Matches 28; Conservative 3; Mismatches 9; Indels 2; Gaps 1;

QY 1 MLSNRLILLNKAALRKAHTSMVRNFRYKPKVQS--OLKPRDL 40

DB 1 MLFNRLILLNNAAFNGHNFVRNRCGQPLQNKVQLKGRDL 42

RESULT 4

152779

ornithine transcarbamylase peptide - rat (fragment)

C:Species: Rattus sp. (rat)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 18-Jun-1999

C:Accession: 152779

R:Horwich, A.L.; Kalousek, F.; Fenton, W.A.; Pollock, R.A.; Rosenberg, L.E.

Cell 44, 451-459, 1986

A:Title: Targeting of pre-ornithine transcarbamylase to mitochondria: Definition of crit

A:Reference number: 152779; MUID:86106223; PMID:3943133

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-41 <RES>

C:Cross-references: GB:M12583; NID:g205887; PIDN:AAA41770.1; PID:g205888

C:Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase

Query Match

Best Local Similarity

Matches 22; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MLSNRLILLNKAALRKAHTSMVRNFRYKPKVQSOLK 36

DB 1 MLFNRLILLNNAAFNGHNFVRNRCGQPLQNKVQ 36

RESULT 5

A48421

ornithine transcarbamylase - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999

C:Accession: A48421

R:Helbing, C.; Gergely, G.; Atkinson, B.G.

Dev. Genet. 13, 289-301, 1992

A:Title: Sequential up-regulation of thyroid hormone beta receptor, ornithine transcarba

d thyroid hormone-induced metamorphosis.

A:Reference number: A48421; MUID:93177976; PMID:1291156

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-350 <HEL>

A:Cross-references: GB:M95193; NID:g213683; PIDN:AAA49528.1; PID:g213684

A:Experimental source: liver

A:Note: sequence extracted from NCBI backbone (NCBIN:126154, NCBIP:126155)

C:Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase

C:Keywords: mitochondrion

F:36-338/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>

Query Match

Best Local Similarity

Matches 16; Conservative 9; Mismatches 13; Indels 2; Gaps 2;

27.4%; Score 57; DB 2; Length 350;

40.0%; Pred. No. 3.3;

Matches 16; Conservative 9; Mismatches 13; Indels 2; Gaps 2;

27.4%; Score 56; DB 2; Length 1286;

35.3%; Pred. No. 19;

Matches 12; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

26.9%; Score 56; DB 2; Length 1286;

35.3%; Pred. No. 19;

Matches 12; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

26.9%; Score 56; DB 2; Length 1286;

QY 1 MLSNRLILLNKAALRKAHTSMVRNFRYKPKVQSOLKPRDL 40

DB 1 MLHHMRTIIN-ASWRYGKNCIVRQFGFSQ-TYSOLKGRDL 38

RESULT 6

P90409

GTP binding conserved hypothetical protein SSO3385 [imported] - Sulfolobus solfatar

C:Species: Sulfolobus solfataricus

C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C:Accession: P90409

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awavez, M.J.; C

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redde

arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: P90409

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-351 <KUR>

A:Cross-references: GB:AE006641; NID:gl3815687; PIDN:AAK42533.1; GSPDB:GN00155

C:Genetics:

A:Gene: SSO2385

Query Match 27.4%; Score 57; DB 2; Length 351;

Best Local Similarity 32.7%; Pred. No. 3.3;

Matches 17; Conservative 8; Mismatches 9; Indels 18; Gaps 3;

QY 7 ILINKAA-----LRKAHTSMVRNFRY----GRPVQSQ-----LKPRDL 40

DB 294 LILKGGTVDLVARKLHSLAENFRYRVWGVKQKGVQKGVSHLEDRDI 345

RESULT 7

B71413

hypothetical protein dl3525w - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

A:Variety: columbia

C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000

C:Accession: B71413

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.;

P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weizenecker, T.; Pohl, T.M.; Terry, N.;

avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk,

Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdom

erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;

C.; Chalwatzis, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis

A:Reference number: A71400; MUID:98121113; PMID:9461215

A:Accession: B71413

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1286 <BEV>

A:Cross-references: GB:Z97337; NID:g2244829; PID:g2244854

C:Genetics:

A:Map position: 4COP9-4G3845

C:Superfamily: Arabidopsis thaliana hypothetical protein dl3525w

Query Match

Best Local Similarity

Matches 12; Conservative

8; Mismatches 14; Indels

0; Gaps 0;

26.9%; Score 56; DB 2; Length 1286;

35.3%; Pred. No. 19;

Matches 12; Conservative

8; Mismatches 14; Indels

0; Gaps 0;

26.9%; Score 56; DB 2; Length 1286;

35.3%; Pred. No. 19;

Matches 12; Conservative

8; Mismatches 14; Indels

0; Gaps 0;

26.9%; Score 56; DB 2; Length 1286;

35.3%; Pred. No. 19;

Matches 12; Conservative

8; Mismatches 14; Indels

0; Gaps 0;

26.9%; Score 56; DB 2; Length 1286;

35.3%; Pred. No. 19;

Matches 12; Conservative

8; Mismatches 14; Indels

0; Gaps 0;

RESULT 8

S58250

DNA-directed DNA polymerase (EC 2.7.7.7) - yeast (Saccharomyces cerevisiae)

N:Alternate names: DNA polymerase I; protein N2181; protein YNL102W

C:Species: Saccharomyces cerevisiae

[illegible]

Fri Jul 25 10:14:03 2003

A:Residues: 1-314 <WHI>
A:Cross-references: GB:AE001913; GB:AE000513; NID:96458240; PIDN:AAF10127.1; PID:9645824
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0548
A:Map position: 1

Query Match 24.8%; Score 51.5; DB 2; Length 314;
Best Local Similarity 43.8%; Pred. No. 18;
Matches 14; Conservative 4; Mismatches 9; Indels 5; Gaps 2;

QY 7 ILINKAALRKKAHTSMVRNFRYKGPVQSOLKPR 38
Db 85 VLSQKAQARPAG---QNERWG-PTQGNVKPR 111

Search completed: July 24, 2003, 22:08:06
Job time : 16.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 24, 2003, 21:59:48 ; Search time 7.32143 Seconds
(without alignments)
263.350 Million cell updates/sec

Title: US-08-765-244-1

Perfect score: 208

Sequence: 1 MLSNRLILNKAALKAHTS.....VRFNRYKPVQSLKPRDLCL 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	179	86.1	354	1	OTC_RAT
2	144	69.2	354	1	OTC_MOUSE
3	125	60.1	354	1	OTC_HUMAN
4	57	27.4	350	1	OTC_RANCA
5	55.5	26.7	1468	1	DPOA_YEAST
6	54	26.0	236	1	R82_LOTJA
7	53	25.5	435	1	C8S5_YEAST
8	53	25.5	597	1	IF2P_METAC
9	52.5	25.2	185	1	EFPL_CHLMU
10	51	24.5	226	1	COLI_ONCKE
11	51	24.5	240	1	COLI_ONCKY
12	51	24.5	506	1	POFB_SCHPO
13	50	24.0	591	1	IF2P_METNA
14	50	24.0	593	1	STB2_HUMAN
15	50	24.0	641	1	HRPK_PSESY
16	49	23.6	530	1	TRPG_ECOLI
17	49	23.6	552	1	US1C_HUMAN
18	49	23.6	985	1	INVA_YERPS
19	49	23.6	1739	1	DOTL_HUMAN
20	48.5	23.3	1114	1	RFT_HUMAN
21	48	23.1	88	1	R37A_SCHPO
22	48	23.1	260	1	PSMA_PIRAB
23	48	23.1	260	1	PSMA_PYRHO
24	48	23.1	578	1	SYR_BUCBP
25	47.5	22.8	333	1	Y376_BUCAP
26	47.5	22.8	548	1	NRM1_SHEEP
27	47.5	22.8	906	1	SECA_RICPR
28	47.5	22.8	1110	1	CYGD_BOVIN
29	47	22.6	90	1	R37B_SCHPO
30	47	22.6	260	1	PSMA_PYRFU
31	47	22.6	264	1	UZAG_DROME
32	47	22.6	337	1	NEU1_YEAST
33	47	22.6	748	1	SUF2_HUMAN

34 47 22.6 836 1 YGL1_SCHPO Q9Y7J8 schizosacch
35 47 22.6 905 1 AT58_MOUSE P57110 mus musculu
36 47 22.6 1050 1 ULK1_HUMAN O75385 homo sapien
37 46.5 22.4 385 1 PGK_HAEIN P43726 haemophilus
38 46.5 22.4 429 1 TRB2_SULSO Q97TX6 sulfolobus
39 46.5 22.4 1475 1 N153_HUMAN P49790 homo sapien
40 46 22.1 177 1 MSRA_SULSO Q97Y45 sulfolobus
41 46 22.1 260 1 PSMA_THERK1 O24733 thermococcu
42 46 22.1 305 1 FMT_CAMJE Q9PJ28 campylobact
43 46 22.1 333 1 TRPD_YERPE Q8ZEG7 yersinia pe
44 46 22.1 443 1 CGLH_XANNA P37126 xanthomonas
45 46 22.1 647 1 PRCA_ANAVA P23916 anabaena va

ALIGNMENTS

RESULT 1
OTC_RAT
ID OTC_RAT STANDARD; PRT; 354 AA.
AC P00481; Q63407;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ornithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
DE (OTCase) (Ornithine transcarbamylase).
GN OTC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85063800; PubMed=6095294;
RA Takiguchi M., Miura S., Mori M., Tatibana M., Nacata S., Kaziro Y.;
RT "Molecular cloning and nucleotide sequence of cDNA for rat ornithine
RT carbamoyltransferase precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:7412-7416(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; Tissue=Liver;
RX MEDLINE=87317609; PubMed=3476935;
RA Takiguchi M., Murakami T., Miura S., Mori M.;
RT "Structure of the rat ornithine carbamoyltransferase gene, a large, x
RT chromosome-linked gene with an atypical promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6136-6140(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85215524; PubMed=3839075;
RA Kraus J.P., Hodges P.E., Williamson C.L., Horwich A.L., Kalousek F.,
RA Williams K.R., Rosenberg L.E.;
RT "A cDNA clone for the precursor of rat mitochondrial ornithine
RT transcarbamylase: comparison of rat and human leader sequences and
RT conservation of catalytic sites.";
RL Nucleic Acids Res. 13:943-952(1985).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=85203360; PubMed=3839931;
RA McIntyre P., Graf L., Mercer J.F.B., Wake S.A., Hudson P.J.,
RA Hoogenraad N.;
RT "The primary structure of the imported mitochondrial protein,
RT ornithine transcarbamylase from rat liver: mRNA levels during
RT ontogeny.";
RL DNA 4:147-156(1985).
RN [5]
RP SEQUENCE OF 33-56; 293-302; 307-317 AND 321-329.
RC TISSUE=Liver;
RX MEDLINE=88266748; PubMed=3390141;
RA Aoki Y., Sunaga H., Suzuki K.T.;
RT "A cadmium-binding protein in rat liver identified as ornithine
RT carbamoyltransferase.";
RL Biochem. J. 250:735-742(1988).
CC -l- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate

```

CC CC + L-citrulline.
CC CC -|- PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
CC CC -|- SUBUNIT: Homotrimer.
CC CC -|- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC CC -|- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
CC CC -----
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CC CC -----
CC CC EMBL; K03040; AAA41768.1; -
CC CC EMBL; M16933; AAA41769.1; -
CC CC EMBL; M16924; AAA41769.1; JOINED.
CC CC EMBL; M16925; AAA41769.1; JOINED.
CC CC EMBL; M16926; AAA41769.1; JOINED.
CC CC EMBL; M16928; AAA41769.1; JOINED.
CC CC EMBL; M16929; AAA41769.1; JOINED.
CC CC EMBL; M16930; AAA41769.1; JOINED.
CC CC EMBL; M16932; AAA41769.1; JOINED.
CC CC EMBL; M16933; AAA41769.1; JOINED.
CC CC EMBL; X01976; CAA26007.1; -
CC CC EMBL; K00001; AAA41772.1; -
CC CC EMBL; M11266; AAA41767.1; -
CC CC PIR; A00563; OWRT.
CC CC HSP; P00480; IOTH.
CC CC InterPro; IPR006130; Asp/Orn_Cotransf.
CC CC InterPro; IPR002292; Orn_carbtransf.
CC CC InterPro; IPR006131; OTCace_O.
CC CC InterPro; IPR006132; OTCace_P.
CC CC Pfam; PF00185; OTCace_N; 1.
CC CC Pfam; PF02729; OTCace_N; 1.
CC CC PRINTS; PR00100; AOTCASE.
CC CC TIGRfams; TIGR00658; orn_carb.tr; 1.
CC CC PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
CC CC Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
CC CC Transit peptide.
CC CC TRANSIT 1 32 MITOCHONDRION.
CC CC CHAIN 33 354 ORNITHINE CARBAMOYLTRANSFERASE.
CC CC ACT_SITE 263 263 BY SIMILARITY.
CC CC ACT_SITE 303 303 BY SIMILARITY.
CC CC CONFLICT 39 39 G -> P (IN REF. 3; AAA41772).
CC CC CONFLICT 241 241 G -> S (IN REF. 3).
CC CC SEQUENCE 354 AA; 39886 MW; 156B511AF7063F0C CRC64;
CC CC -----
CC CC Query Match 86.1%; Score 179; DB 1; Length 354;
CC CC Best Local Similarity 92.9%; Pred. No. 2.1e-18;
CC CC Matches 39; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
CC CC -----
CC CC QY 1 MLSNRLILNKAALRKAKHTSMVRNFRYKGPVQS--QLKPRDL 40
CC CC ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC CC Db 1 MLSNRLILNKAALRKAKHTSMVRNFRYKGPVQSQVLKGRDL 42
CC CC -----
CC CC RESULT 2
CC CC OTC_MOUSE
CC CC ID OTC_MOUSE STANDARD; PRT; 354 AA.
CC CC AC P11725;
CC CC DT 01-OCT-1989 (Rel. 12, Created)
CC CC DT 01-OCT-1989 (Rel. 12, Last sequence update)
CC CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC CC DE Ornithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
CC CC (Otcase) (ornithine transcarbamylase).
CC CC OTC.
CC CC OS Mus musculus (Mouse).
CC CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC CC OX NCBI_TaxID=10090;
CC CC RN [1]
CC CC RP SEQUENCE FROM N.A.
CC CC RC STRAIN=C57BL/6J;

```

```

RX MEDLINE=87263407; PubMed=3603027;
RA Veres G., Gibbs R.A., Scherer S.E., Caskey C.T.;
RT "The molecular basis of the sparse fur mouse mutation.";
RL Science 237:415-417(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8815717; PubMed=2831503;
RA Scherer S.E., Veres G., Caskey C.T.;
RT "The genetic structure of mouse ornithine transcarbamylase.";
RL Nucleic Acids Res. 16:1593-1601(1988).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=86224037; PubMed=3011788;
RA Veres G., Craigen W.J., Caskey C.T.;
RT "The 5' flanking region of the ornithine transcarbamylase gene
contains DNA sequences regulating tissue-specific expression.";
RL J. Biol. Chem. 261:7588-7591(1986).
CC -|- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
+ L-citrulline.
CC -|- PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
CC -|- SUBUNIT: Homotrimer.
CC -|- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -|- DISEASE: SPARSE FUR (SPF) MOUSE HAVE AN OTC WITH AN OVERALL
DECREASE IN ACTIVITY, AND ALTERED SUBSTRATE AFFINITY.
CC -|- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
CC -----
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CC CC -----
CC CC EMBL; M17030; AAA39865.1; -
CC CC EMBL; M12716; AAA39864.1; ALT_SEQ.
CC CC EMBL; X07092; CAA30121.1; -
CC CC EMBL; X07093; CAA30121.1; JOINED.
CC CC EMBL; X07094; CAA30121.1; JOINED.
CC CC EMBL; X07095; CAA30121.1; JOINED.
CC CC EMBL; X07096; CAA30121.1; JOINED.
CC CC EMBL; X07097; CAA30121.1; JOINED.
CC CC EMBL; X07098; CAA30121.1; JOINED.
CC CC EMBL; X07099; CAA30121.1; JOINED.
CC CC EMBL; X07100; CAA30121.1; JOINED.
CC CC PIR; A43609; OWMS.
CC CC HSP; P00480; IOTH.
CC CC SWISS-2DPAGE; P11725; MOUSE.
CC CC MGD; MGI:97448; Otc.
CC CC InterPro; IPR006130; Asp/Orn_Cotransf.
CC CC InterPro; IPR002292; Orn_carbtransf.
CC CC InterPro; IPR006131; OTCace_O.
CC CC InterPro; IPR006132; OTCace_P.
CC CC Pfam; PF00185; OTCace_N; 1.
CC CC Pfam; PF02729; OTCace_N; 1.
CC CC PRINTS; PR00100; AOTCASE.
CC CC TIGRfams; TIGR00658; orn_carb.tr; 1.
CC CC PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
CC CC Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
CC CC Transit peptide.
CC CC TRANSIT 1 32 MITOCHONDRION.
CC CC CHAIN 33 354 ORNITHINE CARBAMOYLTRANSFERASE.
CC CC ACT_SITE 263 263 BY SIMILARITY.
CC CC ACT_SITE 303 303 BY SIMILARITY.
CC CC VARIANT 117 117 H -> N (IN SPARSE FUR MOUSE).
CC CC CONFLICT 195 195 G -> R (IN REF. 2).
CC CC SEQUENCE 354 AA; 39765 MW; 33BB5D1E88AA196 CRC64;
CC CC -----
CC CC Query Match 69.2%; Score 144; DB 1; Length 354;
CC CC Best Local Similarity 78.6%; Pred. No. 2.6e-13;
CC CC Matches 33; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

```


Hum. Genet. 91:321-325(1993).
[18]
RP VARIANTS OTCD LEU-117; LEU-182 AND CYS-203.
RP MEDLINE=94290509; PubMed=8019569;
RX Tuchman M., Plante R.J., Giguere Y., Lemieux B.,
RA "The ornithine transcarbamylase gene: new 'private' mutations in four
RT patients and study of a polymorphism.",
RL Hum. Mutat. 3:318-320(1994).
RP VARIANTS
RP VARIANTS OTCD GLY-126; HIS-129 AND MET-172.
RP MEDLINE=94362715; PubMed=6081398;
RA Matsura T., Hoshide R., Kiwaki K., Komaki S., Koike E., Endo F.,
RA Oyanagi K., Suzuki Y., Kato I., Ishikawa K., Yoda H., Kamitani S.,
RA Sakaki Y., Matsuda I.,
RT "Four newly identified ornithine transcarbamylase (OTC) mutations
RT (D126G, R125H, I172M and W32X) in Japanese male patients with early-
RT onset OTC deficiency.",
RL Hum. Mutat. 3:402-406(1994).
RP VARIANTS
RP VARIANTS OTCD HIS-40; HIS-129; ARG-195; THR-225; GLN-277 AND
RP GLU-309 DEL.
RP MEDLINE=95038770; PubMed=7951259;
RX Tuchman M., Plante R.J., McCann M.T., Qureshi A.A.,
RA "Seven new mutations in the human ornithine transcarbamylase gene.",
RL Hum. Mutat. 4:57-60(1994).
[21]
RP VARIANTS OTCD THR-159 AND VAL-209.
RP MEDLINE=96070988; PubMed=8530002;
RA Garcia-Perez M.A., Sanjurjo P., Briones P., Garcia-Munoz M.J.,
RA Rubio V.,
RT "A splicing mutation; a nonsense mutation (Y167X) and two missense
RT mutations (I159T and A209V) in Spanish patients with ornithine
RT transcarbamylase deficiency.",
RL Hum. Genet. 96:549-551(1995).
[22]
RP VARIANTS OTCD GLU-269.
RP MEDLINE=96086561; PubMed=7474905;
RA Zimmer K.P., Matsura T., Colombo J.-P., Koch H.G., Ullrich K.,
RA Deufel T., Harms E., Matsuda I.,
RA "A novel point mutation at codon 269 of the ornithine
RT transcarbamylase (OTC) gene causing neonatal onset of OTC
RT deficiency.",
RL J. Inherit. Metab. Dis. 18:356-357(1995).
[23]
RP VARIANTS OTCD MET-125; ARG-188; VAL-209 AND LEU-302.
RP MEDLINE=96400964; PubMed=8807340;
RX Gilbert-Dussardier B., Segues B., Rozet J.-M., Rabier D., Calvas P.,
RA de Lumley L., Bonnefond J.-P., Munnich A.,
RA "Partial duplication [dup. TCAC (178)] and novel point mutations
RT (T125M, G188R, A209V, and W302L) of the ornithine transcarbamylase
RT gene in congenital hyperammonemia.",
RL Hum. Mutat. 8:74-76(1996).
[24]
RP VARIANTS OTCD HIS-40; ASN-88; TYR-202 AND ASN-263.
RP Guardamagna O., Gatti E., Parini R., Plante R.J., Tuchman M.,
RA "Genotype-phenotype correlations in ornithine transcarbamylase
RT deficiency.",
RL Enzyme Protein 49:191-191(1996).
[25]
RP VARIANTS OTCD ASN-88; CYS-176; ALA-220; TYR-302 AND LYS-343.
RP MEDLINE=97114289; PubMed=8956038

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Query Match          60.1%  Score 125;  DB 1;  Length 354;
Best Local Similarity 66.7%;  Pred. No. 1.5e-10;
Matches 28;  Conservative 3;  Mismatches 9;  Indels 2;  Gaps 1;

QY  1  MLSNRLIILNKAALRKAAHTSMVNFNRYGKPVDS--OLKPRDL 40
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  1  MLENRLIILNNAAPNGHNENFWNFCGQPLONKVKQLGRDL 42
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 4
OTC_RANCA

BEST LOCAL SIMILARITY 40.0%; Pred.: NO. 1.1;
 Matches 16; Conservative 9; Mismatches 13; Indels 2; Gaps 2;

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OTC_RANCA STANDARD; PRT; 350 AA.
P31326;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ornithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
(OTCase) (Ornithine transcarbamylase).
Rana catesbeiana (Bull. frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
NCBI_TaxID=8400;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=93177976; PubMed=1291156;
RA Helbing C., Gergely G., Atkinson B.G.;
RA "Sequential up-regulation of thyroid hormone beta receptor, ornithine
RT transcarbamylase, and carbamyl phosphate synthetase mRNAs in the
RT liver of Rana catesbeiana tadpoles during spontaneous and thyroid
RT hormone-induced metamorphosis.";
RL Dev. Genet. 13:289-301(1992).
[2]
SEQUENCE FROM N.A.
RP Iwase K., Yamauchi K., Ishikawa K.;
RA "Molecular cloning of bullfrog (Rana catesbeiana) ornithine
RT transcarbamylase and induction of its mRNA during spontaneous
RT metamorphosis.";
RL Rep. Fac. Sci. Shizuoka Univ. 29:45-54(1995).
CC -!- FUNCTION: OTC IS NECESSARY FOR THE TADPOLES TRANSITION FROM AN
CC AMMONIOTELIC, AQUATIC LARVA TO A UREOTELIC, TERRESTRIAL ADULT.
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
CC + L-citrulline.
CC -!- PATHWAY: SECOND STEP IN UREA CYCLE, ARGinine BIOSYNTHESIS.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- TISSUE SPECIFICITY: LIVER.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYONIC DEVELOPMENT.
CC -!- INDUCTION: BY thyroid hormone.
CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
CC
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CC
CC EMBL; M95193; AAA49528.1; -
CC EMBL; D38304; BAA22775.1; -
CC PIR; A48421; A48421.
CC HSP; P00480; 10TH.
CC InterPro; IPR006130; Asp/Orn_Cotranf.
CC InterPro; IPR002292; Orn_carbtransf.
CC InterPro; IPR006131; OTCace_O.
CC InterPro; IPR006132; OTCace_P.
CC Pfam; PF00185; OTCace; 1.
CC Pfam; PF02729; OTCace_N; 1.
CC PRINTS; P000100; ATCASE.
CC TIGRfams; TIGR00658; Orni_carb_tr; 1.
CC PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
CC Arginine biosynthesis; Urea cycle; Transferrase; Mitochondrion;
CC Trans. peptide.
CC TRANSIT 1 30 MITOCHONDRION (BY SIMILARITY).
CC CHAIN 31 350 ORNITHINE CARBAMOYLTRANSFERASE.
CC ACT_SITE 259 259 BY SIMILARITY.
CC ACT_SITE 299 299
CC SEQUENCE 350 AA; 39636 MW; EIE598355F03C13E CRC64;
SQ

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Query Match 27.4%; Score 57; DB 1; Length 350;
Best Local Similarity 40.0%; Pred. No. 1.1;
Matches 16; Conservative 9; Mismatches 13; Indels

```

QY 1 MLSNRLILNKAALKAHTSMVRNFRYKPVQSOLKPRDL 40
   ||::||::||::||::||::||::||::||::||::||
Db 1 MLHHMRTIIN-ASWRYGNKCIYRQFGFSQ-TYSOLKGRDL 38

RESULT 5
DPOA_YEAST STANDARD: PRT; 1468 AA.
AC F13382;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase alpha catalytic subunit (EC 2.7.7.7) (DNA polymerase
DE 1).
GN POL1 OR CDC17 OR YNL102W OR N2181.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
OX [1]
RN
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF GLY-493.
RX MEDLINE=68234507; PubMed=3287376;
RA Pizzagalli A., Valsasinni P., Plevani P., Lucchini G.;
RA "DNA polymerase I gene of Saccharomyces cerevisiae: nucleotide
RT sequence, mapping of a temperature-sensitive mutation, and protein
RT homology with other DNA polymerases.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:3772-3776(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=5288c//FY1679;
RX MEDLINE=5288c//FY1679;
RX STRAIN=5288c//FY1679; PubMed=8701612;
RA Saiz J.E., Butrago M.J., Soler A., del Rey F., Revuelta J.L.;
RA "The sequence of a 21.3 kb DNA fragment from the left arm of yeast
RT chromosome XIV reveals LEU4, MEH4, POL1, RAS2, and six new open
RT reading frames.";
RL Yeast 12:403-409(1996).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=5288c;
RX MEDLINE=93188702; PubMed=8446029;
RA Mountain H.A., Bystroem A.S., Korch C.;
RA "The general amino acid control regulates MEH4, which encodes a
RT methionine-pathway-specific transcriptional activator of
RT Saccharomyces cerevisiae.";
RL Mol. Microbiol. 7:215-228(1993).
RN [4]
RP FUNCTION, AND SUBUNIT.
RC MEDLINE=20357110; PubMed=10896792;
RA Qi H., Zakian V.A.;
RA "The Saccharomyces telomere-binding protein Cdc13p interacts with both
RT the catalytic subunit of DNA polymerase alpha and the telomerase-
RT associated est1 protein.";
RL Genes Dev. 14:1777-1788(2000).
CC -1- FUNCTION: Polymerase alpha in a complex with DNA primase is a
CC replicative polymerase. Has a role in promoting telomere
CC replication during interaction with CDC13.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
CC + [DNA](N).
CC -1- SUBUNIT: Interacts with CDC13.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- MISCELLANEOUS: In eukaryotes there are five DNA polymerases:
CC alpha, beta, gamma, delta, and epsilon which are responsible for
CC different reactions of DNA synthesis.
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
CC
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RA Kawauchi H., Adachi Y., Tsubokawa M.;
 RT "Occurrence of a new melanocyte stimulating hormone in the salmon
 RL pituitary gland.";
 RL Biochem. Biophys. Res. Commun. 96:1508-1517(1980).
 RN [5]
 RP SEQUENCE OF 198-226.
 RX MEDLINE=79255548; PubMed=475783;
 RA Kawauchi H., Tsubokawa M., Muramoto K.;
 RT "Isolation and primary structure of endorphin from salmon pituitary
 RL glands.";
 RL Biochem. Biophys. Res. Commun. 88:1249-1254(1979).
 CC -1- PFM: SPECIFIC ENZYMAIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
 CC THE DIFFERENT ACTIVE PEPTIDES.
 CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M27692; AAA49426.1; ALT_INIT.
 DR EMBL: K02613; AAA49424.1; .
 DR EMBL: K02614; AAA49425.1; .
 DR EMBL: X01122; CAA25591.1; .
 DR PIR: I51080; CTONPK.
 DR InterPro: IPR001941; Mcoirtin_ACTH.
 DR Pfam: PF00976; ACTH_domain; 1.
 DR PRINTS: PR00383; MELANOCORTIN.
 DR PRODOM: PD003250; Mcoirtin_ACTH; 1.
 KW Endorphin; Hormone; Cleavage on pair of basic residues; Acetylation;
 KW Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT PEPTIDE 98 138 CORTICOTROPIN.
 FT PEPTIDE 98 112 MELANOTROPIN ALPHA.
 FT PEPTIDE 116 138 CORTICOTROPIN-LIKE INTERMEDIARY PEPTIDE.
 FT PEPTIDE 141 226 LIPOTROPIN BETA.
 FT PEPTIDE 141 195 LIPOTROPIN GAMMA.
 FT PEPTIDE 179 195 MELANOTROPIN BETA.
 FT PEPTIDE 198 226 BETA-ENDORPHIN.
 FT PEPTIDE 198 202 MET-ENKEPHALIN.
 FT MOD_RES 98 98 ACETYLATION.
 SQ SEQUENCE 226 AA; 24982 MW; 327CA785F69B1B24 CRC64;
 Query Match 24.5%; Score 51; DB 1; Length 226;
 Best Local Similarity 36.4%; Pred. No. 5;
 Matches 8; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 QY 16 KAHTSMVRNFRYKPKVQSQLKP 37
 ID COLJ_ONCMY STANDARD; PRT; 240 AA.
 AC Q04618;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Corticotropin-lipotropin B precursor (Pro-opiomelanocortin) (POMC).
 GN POMC-B.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=93078794; PubMed=1448114;

RA Salbert G., Chauveau I., Bonnet G., Valotaire Y., Jégo P.;
 RT "One of the two trout proopiomelanocortin messenger RNAs potentially
 RL encodes new peptides.";
 RL Mol. Endocrinol. 6:1605-1613(1992).
 CC -1- TISSUE SPECIFICITY: PITUITARY AND HYPOTHALAMUS OF ADULT DIPLOID
 CC ANIMALS.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED ONLY IN SEXUALLY ACTIVE FISH.
 CC -1- PFM: SPECIFIC ENZYMAIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
 CC THE DIFFERENT ACTIVE PEPTIDES.
 CC -1- PFM: ACETYLATION OF BETA-ENDORPHIN OCCURS IN A TISSUE-SPECIFIC
 CC MANNER.
 CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-15 IS THE INITIATOR.
 CC -----
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 CC -----
 DR EMBL: X69809; CAA49467.1; .
 DR PIR: B45359; B45359.
 DR InterPro: IPR001941; Mcoirtin_ACTH.
 DR Pfam: PF00976; ACTH_domain; 1.
 DR PRODOM: PD003250; Mcoirtin_ACTH; 1.
 KW Endorphin; Hormone; Cleavage on pair of basic residues; Amidation;
 KW Signal; Acetylation; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 36 POTENTIAL.
 FT PEPTIDE 37 108 NPP 2 (BY SIMILARITY).
 FT PEPTIDE 112 152 CORTICOTROPIN (ACTH) (BY SIMILARITY).
 FT PEPTIDE 112 124 MELANOTROPIN ALPHA 2 (ALPHA-MSH 2)
 FT PEPTIDE 130 152 (BY SIMILARITY).
 FT PEPTIDE 130 152 CORTICOTROPIN-LIKE INTERMEDIARY PEPTIDE 2
 FT PEPTIDE 155 240 (CLIP 2) (BY SIMILARITY).
 FT PEPTIDE 155 240 LIPOTROPIN BETA (LPH-BETA)
 FT PEPTIDE 155 209 (BY SIMILARITY).
 FT PEPTIDE 193 209 LIPOTROPIN GAMMA (LPH-GAMMA)
 FT PEPTIDE 212 240 (BY SIMILARITY).
 FT PEPTIDE 212 216 MELANOTROPIN BETA 2 (BETA-MSH 2)
 FT MOD_RES 37 37 MET-ENKEPHALIN.
 FT MOD_RES 112 112 PYRROLIDONE CARBOXYLIC ACID
 FT MOD_RES 124 124 (BY SIMILARITY).
 FT MOD_RES 124 124 ACETYLATION (BY SIMILARITY).
 FT MOD_RES 124 124 AMIDATION (G-125 PROVIDE AMIDE GROUP)
 FT MOD_RES 124 124 (BY SIMILARITY).
 SQ SEQUENCE 240 AA; 26719 MW; 4F715CE8E6424F6C CRC64;
 Query Match 24.5%; Score 51; DB 1; Length 240;
 Best Local Similarity 36.4%; Pred. No. 5.4;
 Matches 8; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 QY 16 KAHTSMVRNFRYKPKVQSQLKP 37
 ID COLJ_ONCMY STANDARD; PRT; 240 AA.
 AC Q04618;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Corticotropin-lipotropin B precursor (Pro-opiomelanocortin) (POMC).
 GN POMC-B.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=93078794; PubMed=1448114;

Search completed: July 24, 2003, 22:04:31
Job time : 10.3214 secs

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OM protein - protein search, using sw model

Run on: July 24, 2003, 22:01:38 ; Search time 29.2857 seconds
(without alignments)
361.274 Million cell updates/sec

Title: US-08-765-244-1

Perfect score: 208

Sequence: 1 MLSNRLINKAALRAKHAHTS.....VNRFRYGRPVQSLKPRDL 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	179	86.1	102	11	P70518	P70518 rattus norv
2	144	69.2	351	11	Q8RIA8	Q8RIA8 mus musculu
3	114	54.8	354	6	Q9N1U7	Q9N1U7 bos taurus
4	112	53.8	41	11	Q63786	Q63786 rattus norv
5	92	44.2	354	13	Q9IAU8	Q9IAU8 trachemys s
6	57	27.4	351	17	Q97W55	Q97W55 sulfolobus
7	56	26.9	356	13	Q9IAV0	Q9IAV0 sceloporos
8	56	26.9	1286	10	O23351	O23351 arabidopsis
9	54.5	26.2	138	16	Q9JUG9	Q9JUG9 neisseria m
10	54	26.0	457	13	Q8AVS9	Q8AVS9 xenopus lae
11	54	26.0	544	5	O56570	O56570 drosophila
12	54	26.0	769	2	Q23393	Q23393 pseudomonas
13	53.5	25.7	260	16	O50746	O50746 borrelia bu
14	53.5	25.7	383	16	Q9KAV8	Q9KAV8 bacillus ha
15	53	25.5	499	2	O8KN7	O8KN7 clostridium
16	52.5	25.2	140	12	Q99A14	Q99A14 bovine vira

17	52.5	25.2	141	16	Q8DG64	Q8DG64 synechococ
18	52.5	25.2	475	5	Q9NGB5	Q9NGB5 drosophila
19	52.5	25.2	942	5	Q95VA4	Q95VA4 drosophila
20	52.5	25.2	1138	5	Q95VA3	Q95VA3 drosophila
21	52.5	25.2	1608	5	Q95VA5	Q95VA5 drosophila
22	51.5	24.8	306	10	Q9S728	Q9S728 arabidopsis
23	51.5	24.8	314	16	Q9RW7	Q9RW7 deinococcus
24	51.5	24.8	346	2	Q9SUJ3	Q9SUJ3 burkholderi
25	51.5	24.8	346	2	Q9AI37	Q9AI37 burkholderi
26	51	24.5	1779	5	O18150	O18150 caenorhabdi
27	50.5	24.3	296	5	Q9VXZ7	Q9VXZ7 drosophila
28	50.5	24.3	755	5	Q9V4J5	Q9V4J5 drosophila
29	50.5	24.3	781	5	Q8IGP7	Q8IGP7 drosophila
30	50	24.0	191	12	Q8JLA0	Q8JLA0 ectromelia
31	50	24.0	211	2	Q9R6K6	Q9R6K6 agrobacteri
32	50	24.0	310	4	Q9EBM4	Q9EBM4 homo sapien
33	50	24.0	318	4	Q96B22	Q96B22 homo sapien
34	50	24.0	376	5	Q8SUE7	Q8SUE7 encephalito
35	50	24.0	465	4	Q9HBM3	Q9HBM3 homo sapien
36	50	24.0	579	4	O00184	O00184 homo sapien
37	50	24.0	590	4	Q9BU65	Q9BU65 homo sapien
38	50	24.0	632	4	Q96JX1	Q96JX1 homo sapien
39	50	24.0	654	4	Q9H6X0	Q9H6X0 homo sapien
40	50	24.0	702	4	Q8I221	Q8I221 homo sapien
41	50	24.0	787	12	Q83944	Q83944 olive laten
42	50	24.0	831	4	Q8NEM5	Q8NEM5 homo sapien
43	50	24.0	866	5	Q9GPC3	Q9GPC3 drosophila
44	50	24.0	866	5	Q9W034	Q9W034 drosophila
45	50	24.0	882	4	Q9HBM5	Q9HBM5 homo sapien

ALIGNMENTS

RESULT 1

P70518 PRELIMINARY; PRT; 102 AA.
ID P70518;
AC P70518;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Ornithine carbamoyltransferase precursor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85051832; Pubmed=6548714;
RA McIntyre P., Graf L., Mercer J., Peterson G., Hudson P.J.,
RA Hoogenraad N.;
RT "A highly basic N-terminal extension of the mitochondrial matrix
enzyme ornithine transcarbamylase from rat liver.";
RL FEBS Lett. 177:41-46(1984).
DR EMBL; K03041; AAA41771.1; -.
DR HSP; P00480; IOTH.
DR InterPro; IPR006130; Asp/Orn_Cotranf.
DR InterPro; IPR006132; OTCace_P.
DR Pfam; PF02729; OTCace_N; 1.
DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
FT SIGNAL; 1 32 POTENTIAL.
FT CHAIN 33 >102 ORNITHINE CARBAMOYLTRANSFERASE.
FT NON_TER 102 102
SQ SEQUENCE 102 AA; 11932 MW; B739C41F19BF720D CRC64;

Query Match 86.1%; Score 179; DB 11; Length 102;
Best Local Similarity 92.9%; Pred. No. 5.3e-19;
Matches 39; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 MLSNRLINKAALRAKHAHTSWNRFRYGRPVQSLKPRDL 40
|||||
Db 1 MLSNRLINKAALRAKHAHTSWNRFRYGRPVQSLKPRDL 42

4


```
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein NMA1316.
GN NMA1316.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=2022555; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Davis K., Feltham D., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RL meningitidis Z494."
RL Nature 404:502-506(2000).
DR EMBL; ALI62755; CAB84568.1; -
DR InterPro; IPR006522; Tail_comp_S.
DR TIGRFAMs; TIGR01635; tail_comp_S; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 138 AA; 15738 MW; FCOEB880236F2113 CRC64;

Query Match 26.2%; Score 54.5; DB 16; Length 138;
Best Local Similarity 42.9%; Pred. No. 3.9;
Matches 15; Conservative 4; Mismatches 15; Indels 1; Gaps 1;

QY 6 RLLNKAALRKHAHTSMVRNFRY-GKPVQSQLKPRD 39
DB 25 RYLLMRLLSETMHTAVKLNFRYAGRPKGLKYRD 60

RESULT 10
Q8AVS9 PRELIMINARY; PRT; 457 AA.
AC Q8AVS9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to hypothetical protein MGC11993.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RA Submitted (DEC-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC041284; AAH41284.1; -
KW Hypothetical protein.
SQ SEQUENCE 457 AA; 51021 MW; EE44FB225DD0039B CRC64;

Query Match 26.0%; Score 54; DB 13; Length 457;
Best Local Similarity 46.4%; Pred. No. 18;
Matches 13; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 2 LSNRLILLNKAALRKHAHTSMVRNFRYK 29
DB 135 LWDLRLKNSKACTLHGHTSWKNIEYDK 162

RESULT 11
O96570 PRELIMINARY; PRT; 544 AA.
AC O96570;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE 37CS protein (Protein CS).
GN CG10561 OR ANON-37CS OR CS.
OS Drosophila lebanonensis (Fruit fly) (Scaptodrosophila lebanonensis).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Scaptodrosophila.
OX NCBI_TaxID=7225;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BEIRUT;
RX MEDLINE=99250256; PubMed=10231575;
RA Tatarenkov A., Saez A.G., Ayala F.J.;
RT "A compact gene cluster in drosophila: the unrelated Cs gene is
RT compressed between duplicated amd and dac."
RL Gene 231:111-120(1999).
CC -!- FUNCTION: HAS A NONVITAL FUNCTION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
DR EMBL; AF091329; AAC67584.1; -
DR Flybase; FBgn0025668; DlebcG10561.
DR InterPro; IPR002937; Amino_Oxidase.
DR InterPro; IPR000205; NAD_Binding.
DR Pfam; PF01593; Amino_oxidase; 1.
SQ SEQUENCE 544 AA; 61026 MW; CF003E2CBB7D6DBE CRC64;

Query Match 26.0%; Score 54; DB 5; Length 544;
Best Local Similarity 37.1%; Pred. No. 21;
Matches 13; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLNRLILLNKAALRKHAHTSMVRNFRYKGPVQSOL 35
DB 332 VLKNEFSAILFKPALPLEKLOAIRNLGYGNPKYIL 366

RESULT 12
Q52393 PRELIMINARY; PRT; 769 AA.
AC Q52393;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE HrpY protein.
GN HRPY.
OS Pseudomonas syringae (pv. phaseolicola).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=319;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Race4;
RX MEDLINE=95178735; PubMed=7873779;
RA Mansfield J., Jenner C., Hockenhull R., Bennett M.A., Stewart R.;
RA Mansfield J., Jenner C., Hockenhull R., Bennett M.A., Stewart R.;
RT "Characterization of avrPphE, a gene for cultivar-specific avirulence
RT from Pseudomonas syringae pv. phaseolicola which is physically linked
RT to hrpY, a new hrp gene identified in the halo-blight bacterium."
RL Mol. Plant Microbe Interact. 7:726-739(1994).
DR EMBL; U16817; AAA67932.1; -
DR EMBL; U16817; AAA67932.1; -
SQ SEQUENCE 769 AA; 80021 MW; 3BDEB3F41942FBB8 CRC64;

Query Match 26.0%; Score 54; DB 2; Length 769;
Best Local Similarity 36.4%; Pred. No. 32;
Matches 12; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 7 ILLNKAALRKHAHTSMVRNFRYKGPVQSOLKPRD 39
DB 448 LVSSDSALQKAVTEQVQNVNSGKALQDLDATD 480

RESULT 13
O50746 PRELIMINARY; PRT; 260 AA.
ID O50746
AC O50746;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
```

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DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Hypothetical protein BBG23.
GN BBG23.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid lp28-2.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uitterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi."
RL Nature 390:580-586(1997).
DR EMBL; AE000786; AAC66071.1; -.
DR TIGR; BBG23; -.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 260 AA; 29807 MW; F3F8905AC8829867 CRC64;

Query Match 25.7%; Score 53.5; DB 16; Length 260;
Best Local Similarity 21.8%; Pred. No. 11;
Matches 12; Conservative 14; Mismatches 10; Indels 19; Gaps 2;

QY 6 RLLNKAALRK-----AHTSMVNRFRYKPKVQS-----OLKPRDLC 41
: : : : : : : : : : : : : : : : : : : : : : : : : :
DB 197 RLVTDYSSIRRDNSWSTGSTSTVTHIEYGEIQSWRYSYKYSGDDTIRPKNTC 251

RESULT 14
Q9KAV8
ID Q9KAV8 PRELIMINARY; PRT; 383 AA.
AC Q9KAV8;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DE 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Short-chain-specific acyl-CoA dehydrogenase.
GN BH2178.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirana C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AF001514; BAB05897.1; -.
DR InterPro; IPR006090; Acyl-CoA_dh_C.
DR InterPro; IPR006091; Acyl-CoA_dh_M.
DR Pfam; PF00441; Acyl-CoA_dh; 1.
DR Pfam; PF02770; Acyl-CoA_dh_M; 1.
KW Complete proteome.
SQ SEQUENCE 383 AA; 42742 MW; E20129A4F567A8C2 CRC64;

Query Match 25.7%; Score 53.5; DB 16; Length 383;
Best Local Similarity 42.9%; Pred. No. 17;
Matches 15; Conservative 3; Mismatches 14; Indels 3; Gaps 1;

QY 2 LSNRLILNKAALRKHTSMVNRFRYKPKVQSOLK 36
: : : : : : : : : : : : : : : : : : : : : : : : : :

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DB 114 IONKQILLNSAATEKATGSPARG---GKPTTTATK 145

RESULT 15
Q8KNN7
ID Q8KNN7 PRELIMINARY; PRT; 499 AA.
AC Q8KNN7;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DE 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DE 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Novyilisin.
GN NVL
OS Clostridium novyi.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1542;
RN [1]
RP SEQUENCE FROM N.A.
RA Cerrato R.R., Valle J.J., Gonzalez-Zorn B.B., Vazquez-Boland J.J.A.;
RT "Clostridium novyi, nvl gene for novyilisin."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ404676; CAC01998.1; -.
DR InterPro; IPR001869; Thiol_cytolysin.
DR Pfam; PF01289; Thiol_cytolysin; 1.
DR PRINTS; PR01400; TACYTOLYSIN.
DR ProDom; PD007062; Thiol_cytolysin; 1.
DR PROSITE; PS00481; THIOL_CYTOLYSINS; 1.
SQ SEQUENCE 499 AA; 55628 MW; 686B917EBC6615F8 CRC64;

Query Match 25.5%; Score 53; DB 2; Length 499;
Best Local Similarity 39.3%; Pred. No. 27;
Matches 11; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 9 LNKALRKHTSMVNRFRYKPKVQSOLK 36
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DB 254 LNKGVSNAPPLMVSNVAYGRPIYVKLE 281

Search completed: July 24, 2003, 22:07:34
Job time : 34.2857 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 24, 2003, 22:02:54 ; Search time 20,9881 seconds
(without alignments)
86,686 Million cell updates/sec

Title: US-08-765-244-22

Perfect score: 217

Sequence: 1 MLSNRLILINKAALRAHTS.....NFRYKPVQSQVLKPRDLC 43

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	42.4	32	2	US-08-373-190-29
2	92	42.4	32	2	US-08-438-190A-29
3	92	42.4	32	3	US-08-350-215-29
4	92	42.4	32	3	US-09-287-145A-29
5	92	42.4	32	4	US-09-556-111-29
6	54	24.9	2539	3	US-09-413-814-42
7	53	24.4	457	4	US-09-252-991A-32812
8	52	24.0	218	4	US-09-252-991A-18053
9	51	23.5	1169	1	US-08-542-921-2
10	51	23.5	1169	2	US-08-880-685-2
11	51	23.5	1169	2	US-08-880-684-2
12	49.5	22.8	208	4	US-09-107-532A-5399
13	49.5	22.8	523	4	US-09-252-991A-18653
14	49.5	22.8	1164	4	US-09-457-708-2
15	49.5	22.8	1164	4	US-09-950-046A-2
16	48	22.1	89	4	US-09-732-210-98
17	47	21.7	20	5	PCT-US95-07543-5
18	47	21.7	91	4	US-09-732-210-195
19	47	21.7	421	3	US-09-002-567B-1
20	47	21.7	421	3	US-09-002-567B-3
21	47	21.7	421	4	US-09-571-347-1
22	47	21.7	421	4	US-09-571-347-3
23	47	21.7	567	3	US-09-188-811-2
24	46.5	21.4	274	4	US-09-252-991A-29653
25	46.5	21.4	582	4	US-09-091-725-17
26	46.5	21.4	659	4	US-09-562-737-16
27	46.5	21.4	1711	3	US-08-365-822C-10

Query Match

42.4% Score 92; DB 2; Length 32;

28 46.5 21.4 1711 3 US-08-582-776C-10 Sequence 10, Appl
29 46.5 21.4 1711 3 US-08-434-831B-10 Sequence 10, Appl
30 46 21.2 559 1 US-08-313-553-15 Sequence 15, Appl
31 46 21.2 559 3 US-08-767-993-15 Sequence 15, Appl
32 46 21.2 729 4 US-09-252-991A-32535 Sequence 32535, A
33 46 21.2 1139 4 US-09-914-259-68 Sequence 68, Appl
34 45.5 21.0 761 4 US-09-585-888-27 Sequence 27, Appl
35 45 20.7 236 4 US-09-252-991A-28901 Sequence 28901, A
36 45 20.7 275 4 US-09-328-352-4817 Sequence 4817, Ap
37 45 20.7 535 4 US-09-312-762A-14 Sequence 14, Appl
38 45 20.7 609 4 US-08-107-532A-5110 Sequence 5110, Ap
39 45 20.7 700 4 US-08-671-757A-10 Sequence 10, Appl
40 45 20.7 716 4 US-09-219-983A-20 Sequence 20, Appl
41 45 20.7 730 1 US-07-846-181-5 Sequence 5, Appl
42 45 20.7 730 1 US-07-845-989-5 Sequence 5, Appl
43 45 20.7 795 4 US-09-252-991A-19085 Sequence 19085, A
44 44 20.7 984 4 US-09-328-352-6926 Sequence 6926, Ap
45 45 20.7 1124 4 US-09-252-991A-26810 Sequence 26810, A

ALIGNMENTS

RESULT 1
US-08-373-190-29
; Sequence 29, Application US/08373190
; Patent No. 5851829
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; APPLICANT: HASELTINE, WILLIAM
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,190
; FILING DATE: 17-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06735
; FILING DATE: 16-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41956-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: STRE UR 2002
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-373-190-29

Best Local Similarity 61.3%; Pred. No. 9.2e-08;
Matches 19; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 MLSNRLILNKAAALRKHAHTSMVRNFRYKPV 31
DB 1 MLFNLRXXLNNAAFRGHGFMVRNFRCGQPL 31

RESULT 2
US-08-438-190A-29
; Sequence 29, Application US/08438190A
; Patent No. 5965371
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; APPLICANT: HASELTINE, WILLIAM
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 12-DEC-1994
; APPLICATION NUMBER: US/08/438,190A
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: EISENSTEIN, RONALD I.
; REGISTRATION NUMBER: 30628
; REFERENCE/DOCKET NUMBER: 41956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-438-190A-29

Query Match 42.4%; Score 92; DB 2; Length 32;
Best Local Similarity 61.3%; Pred. No. 9.2e-08;
Matches 19; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 MLSNRLILNKAAALRKHAHTSMVRNFRYKPV 31
DB 1 MLFNLRXXLNNAAFRGHGFMVRNFRCGQPL 31

RESULT 3
US-08-350-215-29
; Sequence 29, Application US/08350215
; Patent No. 6004940
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE A.
; APPLICANT: RICHARDSON, JENNIFER
; TITLE OF INVENTION: INTRACELLULAR TARGETING OF ENDOGENOUS
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET

CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,215
FILING DATE: 12-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: EISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956-CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-350-215-29

Query Match 42.4%; Score 92; DB 3; Length 32;
Best Local Similarity 61.3%; Pred. No. 9.2e-08;
Matches 19; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 MLSNRLILNKAAALRKHAHTSMVRNFRYKPV 31
DB 1 MLFNLRXXLNNAAFRGHGFMVRNFRCGQPL 31

RESULT 4
US-09-287-145A-29
; Sequence 29, Application US/09287145A
; Patent No. 6072036
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; APPLICANT: HASELTINE, WILLIAM
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/287,145A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/438,190
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: EISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400

RESULT 8
US-09-252-991A-18053
; Sequence 18053, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18053
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18053

Query Match 24.0%; Score 52; DB 4; Length 218;
Best Local Similarity 33.3%; Pred. No. 2.4;
Matches 16; Conservative 6; Mismatches 20; Indels 6; Gaps 1;
QY 1 MSLNRLILLNKAALRK-----AHTSMVRNFRYKPVQSQVOLKPRDL 42
Db 116 MLDLPLKATHAGRRPFISRSTAHLEVGAEHGKPLASLEQUTPREV 163

RESULT 9
US-08-542-921-2
; Sequence 2, Application US/08542921
; Patent No. 5736514
; GENERAL INFORMATION:
; APPLICANT: IIZUKA, TOSHIHIKO
; APPLICANT: TAGAWA, MICHITO
; APPLICANT: ARAI, SATOSHI
; APPLICANT: NIIZEKI, MASATSUGU
; APPLICANT: MIYAKE, TOSHIRO
; TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
; TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/542,921
; FILING DATE: 13-OCT-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 276082/94
; FILING DATE: 14-OCT-1994
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 49-209-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1169 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-542-921-2
Query Match 23.5%; Score 51; DB 1; Length 1169;
Best Local Similarity 25.5%; Pred. No. 28;
Matches 14; Conservative 12; Mismatches 15; Indels 14; Gaps 2;
QY 2 LSNRLILLN-----KAALRKAHTSMVRNFRYG---KPVQSQVOLKPRDL 42
Db 359 LSNLQILVNYQTNGSAWRGSRVRYHYLHSSIIQEKSYGLLSDPVGANINVQNNDI 413
RESULT 10
US-08-880-685-2
; Sequence 2, Application US/08880685
; Patent No. 5834296
; GENERAL INFORMATION:
; APPLICANT: IIZUKA, TOSHIHIKO
; APPLICANT: TAGAWA, MICHITO
; APPLICANT: ARAI, SATOSHI
; APPLICANT: NIIZEKI, MASATSUGU
; APPLICANT: MIYAKE, TOSHIRO
; TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
; TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,685
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/542,921
; FILING DATE: 13-OCT-1995
; APPLICATION NUMBER: JP 276082/94
; FILING DATE: 14-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 49-209-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1169 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-880-685-2
Query Match 23.5%; Score 51; DB 2; Length 1169;
Best Local Similarity 25.5%; Pred. No. 28;
Matches 14; Conservative 12; Mismatches 15; Indels 14; Gaps 2;
QY 2 LSNRLILLN-----KAALRKAHTSMVRNFRYG---KPVQSQVOLKPRDL 42

Db 359 LSNLQILVYQTNQNGSAWGRSVRYHYLHSSIIQKSYGLLSDPVGANINVQNDI 413

RESULT 11

US-08-880-684-2

; Sequence 2, Application US/08880684

; Patent No. 5837526

; GENERAL INFORMATION:

; APPLICANT: IIZUKA, TOSHIHIKO

; APPLICANT: TAGAWA, MICHITO

; APPLICANT: ARAI, SATOSHI

; APPLICANT: NIIZEKI, MASATSUGU

; APPLICANT: MIYAKE, TOSHIRO

; TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL

; TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/880,684

; FILING DATE: 23-JUN-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/542,921

; FILING DATE: 13-OCT-1995

; APPLICATION NUMBER: JP 276082/94

; FILING DATE: 14-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 49-209-0

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 413-3000

; TELEFAX: (703) 413-2220

; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1169 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-880-684-2

Query Match 23.5%; Score 51; DB 2; Length 1169;

Best Local Similarity 25.5%; Pred. No. 28;

Matches 14; Conservative 12; Mismatches 15; Indels 14; Gaps 2;

QY 2 LSNLRILLN-----KKAALRKAHTSMVRNFRYKPVQSOVLKPRDL 42

||||:|||||

Db 359 LSNLQILVYQTNQNGSAWGRSVRYHYLHSSIIQKSYGLLSDPVGANINVQNDI 413

RESULT 12

US-09-107-532A-5399

; Sequence 5399, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7310

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; COMPUTER: PC

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,532A

; FILING DATE: 30-JUN-1998

; APPLICATION NUMBER: 60/085,598

; FILING DATE: 14 May 1998

; APPLICATION NUMBER: 60/051571

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Atinello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 5399:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 208 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: YES

; ORIGINAL SOURCE:

; ORGANISM: Enterococcus faecium

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (8) LOCATION 1...208

; SEQUENCE DESCRIPTION: SEQ ID NO: 5399:

US-09-107-532A-5399

Query Match 22.8%; Score 49.5; DB 4; Length 208;

Best Local Similarity 40.7%; Pred. No. 5.6;

Matches 11; Conservative 4; Mismatches 3; Indels 9; Gaps 1;

QY 10 NKAALRKAHTSMVRNFRYKPVQSOVQ 36

||||:|||||

Db 59 NKA-----QNFYRGKPTPELE 76

RESULT 13

US-09-252-991A-18693

; Sequence 18693, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA;

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 18693

; LENGTH: 523

; TYPE: PPT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-18693

Query Match 22.8%; Score 49.5; DB 4; Length 523;

Best Local Similarity 25.5%; Pred. No. 18;

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2003, 22:01:38 ; Search time 30.7143 seconds
(without alignments)
361.274 Million cell updates/sec

Title: US-08-765-244-22

Perfect score: 217

Sequence: 1 MSLNRLILLNKAALRKAHTS.....NFRYKGPQSQVOLKPRDL 43

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp-archaea.*
- 2: sp-bacteria.*
- 3: sp-fungi.*
- 4: sp-human.*
- 5: sp-invertebrate.*
- 6: sp-mammal.*
- 7: sp-mhc.*
- 8: sp-organelle.*
- 9: sp-phage.*
- 10: sp-plant.*
- 11: sp-rodent.*
- 12: sp-virus.*
- 13: sp-vertebrate.*
- 14: sp-unclassified.*
- 15: sp-virus.*
- 16: sp-bacteriap.*
- 17: sp-archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	199	91.7	102	11 P70518	P70518 rattus norv
2	164	75.6	351	11 Q8RIAB	Q8RIAB mus musculu
3	130	59.9	354	6 Q9N1U7	Q9N1U7 bos taurus
4	119	54.8	41	11 Q63786	Q63786 rattus norv
5	106	48.8	354	13 Q91AU8	Q91AU8 trachemys s
6	70	32.3	356	13 Q91AV0	Q91AV0 sceloporu
7	61	28.1	1286	10 Q23351	Q23351 arabidopsis
8	60	27.6	351	17 Q97W55	Q97W55 sulfolobus
9	57	26.3	354	13 Q9YHY9	Q9YHY9 gallus gall
10	56	25.8	369	2 Q9Z635	Q9Z635 streptococ
11	55.5	25.6	454	10 Q91MN3	Q91MN3 arabidopsis
12	54	24.9	300	5 Q44679	Q44679 caenorhabdi
13	54	24.9	457	13 Q8AVS9	Q8AVS9 xenopus lae
14	54	24.9	544	5 Q96570	Q96570 drosophila
15	54	24.9	866	5 Q9GPG3	Q9GPG3 drosophila
16	54	24.9	866	5 Q9W0E4	Q9W0E4 drosophila

17	54	24.9	1053	5 Q8IRH0	Q8IRH0 drosophila
18	54	24.9	1075	5 Q8IRH1	Q8IRH1 drosophila
19	53.5	24.7	141	16 Q8DG64	Q8DG64 synechococ
20	53.5	24.7	425	2 Q45965	Q45965 coxiella bu
21	53.5	24.7	755	5 Q9V4J5	Q9V4J5 drosophila
22	53.5	24.7	781	5 Q8IGP7	Q8IGP7 drosophila
23	53	24.4	247	10 Q9LQU9	Q9LQU9 oryza sativ
24	53	24.4	593	16 Q8ZC64	Q8ZC64 versinia pe
25	53	24.4	601	16 Q8D0D5	Q8D0D5 versinia pe
26	53	24.4	852	2 Q8KJH4	Q8KJH4 rhizobium l
27	52.5	24.2	140	12 Q99A14	Q99A14 bovine vira
28	52	24.0	213	16 Q9HXS7	Q9HXS7 pseudomonas
29	52	24.0	335	5 Q76719	Q76719 caenorhabdi
30	52	24.0	357	13 Q9IAU9	Q9IAU9 alligator m
31	52	24.0	598	16 Q8FH22	Q8FH22 escherichia
32	52	24.0	1009	5 Q8WQJ6	Q8WQJ6 drosophila
33	52	24.0	3004	5 Q4550	Q4550 drosophila
34	52	24.0	3004	5 Q9VYN8	Q9VYN8 drosophila
35	51.5	23.7	260	16 Q50746	Q50746 borrelia bu
36	51	23.5	226	16 Q8EF28	Q8EF28 shewanella
37	51	23.5	376	5 Q8SUE7	Q8SUE7 encephalito
38	51	23.5	499	2 Q8KNM7	Q8KNM7 clostridium
39	51	23.5	598	16 Q8ZF35	Q8ZF35 salmonella
40	51	23.5	598	16 Q8Z7G1	Q8Z7G1 salmonella
41	51	23.5	633	16 P74554	P74554 synechocyst
42	51	23.5	645	2 Q8S603	Q8S603 bacillus th
43	51	23.5	1779	5 Q18150	Q18150 caenorhabdi
44	50.5	23.3	138	16 Q9JUG9	Q9JUG9 neisseria m
45	50.5	23.3	296	5 Q9VXZ7	Q9VXZ7 drosophila

ALIGNMENTS

RESULT 1

P70518 PRELIMINARY; PRT; 102 AA.
AC P70518;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Ornithine carbamoyltransferase precursor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85051832; PubMed=6548714;
RA McIntyre P., Graf L., Mercer J., Peterson G., Hudson P.J.,
RA Hoogenraad N.;
RT "A highly basic N-terminal extension of the mitochondrial matrix
enzyme ornithine transcarbamylase from rat liver.";
RL FEBS Lett. 177:41-46(1984).
DR EMBL; K03041; AAA41771.1; -;
DR HSSP; P00480; 10TH.
DR InterPro; IPR006130; Asp/Orn_Cotranf.
DR InterPro; IPR006132; Ofcace_P.
DR Pfam; PF07279; Ofcace_N; 1.
KW PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
FT SIGNAL; Transferase.
FT SIGNAL; 1 32 POTENTIAL.
FT CHAIN 33 >102 ORNITHINE CARBAMOYLTRANSFERASE.
FT NON_TER 102 102
SQ SEQUENCE 102 AA; B739D41F19BF720D CRC64;

Query Match 91.7%; Score 199; DB 11; Length 102;
Best Local Similarity 97.6%; Pred. No. 9e-22;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSLNRLILLNKAALRKAHTSMVNRFRYKGPQSQVOLKPRDL 42
|||||
DB 1 MSLNRLILLNKAALRKAHTSMVNRFRYKGPQSQVOLKGRDL 42

```

Q9IAU8
ID Q9IAU8 PRELIMINARY; PRT: 354 AA.
AC Q9IAU8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Ornithine transcarbamylase.
DE OTC.
GN Trachemys scripta elegans.
OS Trachemys scripta elegans.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.
OX NCBI_Taxid=31138;
RN [1]
RP SEQUENCE FROM N.A.
RA Shimogiri T., Koyanagi K., Mannen H., Tsuji S.;
RT "Ornithine transcarbamylase is expressed in uricotelic animals."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AF134846; AAF61410.1;
EMBL: AF134846; AAF61410.1;
DR HSP; P00480; IOTH.
DR InterPro: IPR006130; Asp/Orn_Cotranf.
DR InterPro: IPR002292; Orn_carbtransf.
DR InterPro: IPR006131; OTCace_P.
DR InterPro: IPR006132; OTCace_P.
DR Pfam: PF00185; OTCace; 1.
DR Pfam: PF02729; OTCace_N; 1.
DR PRINTS: PR00100; AOTCACE.
DR TIGRfams: TIGR00658; orn_carb_tr; 1.
DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
SQ SEQUENCE 354 AA; 39956 MW; BD6A2C3AE0F99BE CRC64;

Query Match 48.8%; Score 106; DB 13; Length 354;
Best Local Similarity 52.4%; Pred. No. 2; E-07;

```

Matches 22; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 MLSNRLILNKAAALKAHSMVNFYRGKPVQSQVQLKPRDL 42
DB 1 MLFNRLNLAATLNRSSKQLVQHFPSGQPTNINLKGRDL 42

RESULT 6
Q9IAVO
ID Q9IAVO PRELIMINARY; PRT; 356 AA.
AC Q9IAVO;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Ornithine transcarbamylase.
GN OTC.
OS Sceloporus undulatus (Eastern fence lizard) (Skin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=8520;
RN [1]
RP SEQUENCE FROM N.A.
RA Shimogiri T., Koyanagi K., Mannen H., Tsuji S.;
RT "Ornithine transcarbamylase is expressed in uricotelic animals.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF134844; AAF61408.1; -;
DR HSSP; P00480; IOTH.
DR InterPro; IPR006130; Asp/Oro_Cotransf.
DR InterPro; IPR002292; Orn_carbtransf.
DR InterPro; IPR006131; OTCace.O.
DR InterPro; IPR006132; OTCace.P.
DR Pfam; PF00185; OTCace.1.
DR Pfam; PF02729; OTCace_N; 1.
DR PRINTS; PR00100; AOTCACE.
DR TIGRFAMs; TIGR00658; orn_carb_tr; 1.
DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
SQ SEQUENCE 356 AA; 40399 MW; 01D49CCB93E4BBD1 CRC64;

Query Match 32.3%; Score 70; DB 13; Length 356;
Best Local Similarity 40.9%; Pred. No. 0.063;
Matches 18; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

QY 1 MLSNRLILNKAAALKAHSMVNFYRGKPVQSQVQLKPRDL 42
DB 1 MLFNRLNLAATLNRSSKQLVQHFPSGQPTNINLKGRDL 44

RESULT 7
O23351
ID O23351 PRELIMINARY; PRT; 1286 AA.
AC O23351;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Hypothetical 143.9 kDa protein.
GN AT4G14970.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
RA Bergkamp R., Dirke W., van Staveren M., Stiekema W., Drost L.,
RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,
RA Wedler E., Wambutt R., Weitzengraber T., Pohl T.M., Terry N.,
RA Gieren J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,
RA Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
RA Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A.,

RA Vouklatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,
RA Hilbert H., Duesterhoft A., Moors T., Jones J.D.G., Eneva T.,
RA Paine K., Benes V., Rechman S., Ansoorge W., Cooke R., Berger C.,
RA Delseny M., Voet M., Volckaert G., Mewes H.W., Klosterman S.,
RA Schueller C., Chaiwatiz N.;
RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
Arabidopsis thaliana.";
RL Nature 391:485-488(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; Z97337; CAB10276.1; -;
DR EMBL; AL161540; CAB78539.1; -;
KW Hypothetical protein.
SQ SEQUENCE 1286 AA; 143860 MW; F953B283C53D0DEE CRC64;

Query Match 28.1%; Score 61; DB 10; Length 1286;
Best Local Similarity 38.2%; Pred. No. 5.8;
Matches 13; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 3 SNLRLILNKAAALKAHSMVNFYRGKPVQSQV 36
DB 107 SNLRLILNKAAALKAHSMVNFYRGKPVQSQV 140

RESULT 8
Q97W55
ID Q97W55 PRELIMINARY; PRT; 351 AA.
AC Q97W55;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical GTP binding protein SSO2385.
GN SSO2385.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awey M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erasuo G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006839; AAK42533.1; -;
DR InterPro; IPR004095; TGS_dom.
DR Pfam; PF0824; TGS; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 351 AA; 39916 MW; 046A96BF004865DE CRC64;

Query Match 27.6%; Score 60; DB 17; Length 351;
Best Local Similarity 34.6%; Pred. No. 1.9;
Matches 18; Conservative 8; Mismatches 10; Indels 16; Gaps 3;

QY 7 ILLNKAA-----LRKAHSMVNFYRGKPVQSQV-----LKPRDL 42
DB 294 LILKAGTVLDVARKLHSSLAENFYRVWVSKVFGQKVPSPHILEDRI 345

RESULT 9
Q9VHY9
ID Q9VHY9 PRELIMINARY; PRT; 354 AA.
AC Q9VHY9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Ornithine transcarbamylase precursor (EC 2.1.3.3).
 GN OTC.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BREED WHITE LEHORN; TISSUE=Kidney;
 RA MEDLINE=99011321; PubMed=9792920;
 RA Shimogiri T., Kono M., Mannen H., Mizutani M., Tsuji S.;
 RT "Chicken ornithine transcarbamylase gene, structure, regulation, and
 RT chromosomal assignment: repetitive sequence motif in intron 3
 RT regulates this enzyme activity.";
 RL J. Biochem. 124:962-971(1998).
 DR EMBL; AF065629; AAD12234.1;
 DR EMBL; AF065638; AAD33083.1;
 DR EMBL; AF065630; AAD33083.1;
 DR EMBL; AF065631; AAD33083.1; JOINED.
 DR EMBL; AF065632; AAD33083.1; JOINED.
 DR EMBL; AF065634; AAD33083.1; JOINED.
 DR EMBL; AF065635; AAD33083.1; JOINED.
 DR EMBL; AF065636; AAD33083.1; JOINED.
 DR EMBL; AF065637; AAD33083.1; JOINED.
 DR HSP; P00480; IOTH.
 DR InterPro; IPR006130; Asp/Ori_COTranf.
 DR InterPro; IPR002299; Ori_Carboxyltransf.
 DR InterPro; IPR006131; OTCace.O.
 DR InterPro; IPR006132; OTCace.P.
 DR Pfam; PF00185; OTCace; 1.
 DR Pfam; PF02729; OTCace.N; 1.
 DR PRINTS; PR00100; AOTCASE.
 DR TIGRGRAMS; TIGR00658; orni_carb.tr; 1.
 DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
 DR TRANSFERASE.
 KW Transferase.
 SQ SEQUENCE 354 AA; 40245 MW; 20447180BAD9D4ED CRC64;

 Query Match 26.3%; Score 57; DB 13; Length 354;
 Best Local Similarity 40.5%; Pred. No. 5.5;
 Matches 17; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

 QY 1 MSLNRLINKAALRAKHAHTSMVRNFRYKPVQSQVOLKPRDL 42
 DB 1 MLFNKLYRITKLTQNSKHLPRHFCRGPQNMVCLGRDL 42

 RESULT 10
 Q92635
 ID Q92635 PRELIMINARY; PRT; 369 AA.
 AC Q92635;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Putative glucosyl transferase.
 GN CPS19CS.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99395043; PubMed=10464207;
 RA Morona J.K., Morona R., Paton J.C.;
 RT "Comparative genetics of capsular polysaccharide biosynthesis in
 RT Streptococcus pneumoniae types belonging to serogroup 19.";
 RL J. Bacteriol. 181:5355-5364(1999).
 DR EMBL; AF105116; AAD19925.1;
 DR EMBL; AF105116; AAD19925.1;
 DR InterPro; IPR001296; Glyco.trans_1.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 DR TRANSFERASE.
 KW Transferase.
 SQ SEQUENCE 369 AA; 43229 MW; FCFDFD5C106AC8BE CRC64;

Query Match 25.8%; Score 56; DB 2; Length 369;
 Best Local Similarity 32.5%; Pred. No. 8.1;
 Matches 13; Conservative 9; Mismatches 14; Indels 4; Gaps 1;

QY 4 NLRILINKAALRAKHAHTSMVRNFRYKPVQSQVOLKPRDL 43
 DB 48 NVHKVLRLGIKKSDMSMT---YIKYAEHQVHLSPEVC 83

RESULT 11
 Q9LMN3
 ID Q9LMN3 PRELIMINARY; PRT; 454 AA.
 AC Q9LMN3;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE F1694.13 protein.
 GN F1694.13.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Liu S.X., Sakano H., Yu G., Etgu P., Lee J.M., Lenz C., Pham P.,
 RA Toriumi M., Byun E., Chan A., Chin C., Choi E., Chung M., Altafi H.,
 RA Goldsmith A., Gonzalez A., Liu A., Smith A., Vaysberg M., Altafi H.,
 RA Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.F.,
 RA Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M.,
 RA Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
 RA Federspiel N.A., Theologis A.;
 RT "The sequence of BAC F1694 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC036104; AAF81364.1;
 SQ SEQUENCE 454 AA; 50928 MW; 70BC2ACCC9DBEDCF CRC64;

Query Match 25.6%; Score 55.5; DB 10; Length 454;
 Best Local Similarity 45.2%; Pred. No. 12;
 Matches 14; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY 11 KAALRAKHAHT-SMVRNFRYKPVQSQVOLKPR 40
 DB 422 KAAYSRSTSDSPSRNYRESQPMGSPVQAPR 452

RESULT 12
 Q44679
 ID Q44679 PRELIMINARY; PRT; 300 AA.
 AC Q44679;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical 33.8 kDa protein.
 GN C14C6.13.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX SEQUENCE FROM N.A.
 RA David M., Wohldmann P., Bauer C., Antoniou B.;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: July 24, 2003, 21:59:48 ; Search time 7.67857 Seconds
(without alignments)
263.350 Million cell updates/sec

Title: US-08-765-244-22

Perfect score: 217

Sequence: 1 MLNRLILINKAALRAKHTS.....NERYGKPVQSQVQLKPRDLIC 43

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	199	91.7	354	1	P00481 rattus norv
2	164	75.6	354	1	P11725 mus musculus
3	141	65.0	354	1	Q00480 homo sapien
4	59	27.2	597	1	P08415 methanosarc
5	56	25.8	591	1	Q8PU78 methanosarc
6	53	25.3	350	1	P31326 rana catesb
7	54	24.9	236	1	Q9BBS6 lotus japon
8	54	24.9	457	1	P37129 salmonella
9	54	24.9	1225	1	Q90640 gallus gall
10	53	24.4	328	1	O19072 sus scrofa
11	53	24.4	435	1	P30283 saccharomyc
12	52.5	24.2	185	1	Q9PKR6 chlamydia m
13	52	24.0	598	1	NARX_ECOLI
14	51	23.5	506	1	POFB_SCHPO
15	51	23.5	705	1	YM37_YEAST
16	51	23.5	1169	1	C9DA_BACTP
17	50.5	23.3	429	1	TRB2_SULSO
18	50	23.0	330	1	LARU_VIBPA
19	50	23.0	622	1	SR68_CANFA
20	50	23.0	662	1	PRCA_ANASP
21	49.5	22.8	864	1	RA50_SULSO
22	49.5	22.8	1163	1	TSC1_RAT
23	49.5	22.8	1164	1	TSC1_HUMAN
24	49	22.6	457	1	HENN_ECOLI
25	49	22.6	1219	1	MYSS_YEAST
26	49	22.6	1345	1	YH00_YEAST
27	48.5	22.4	5035	1	RYR1_PIG
28	48.5	22.4	5037	1	RYR1_RABIT
29	48.5	22.4	5038	1	RYR1_HUMAN
30	48	22.1	88	1	R37A_SCHPO
31	48	22.1	578	1	SYR_BUCBP
32	48	22.1	647	1	PRCA_ANAVA
33	48	22.1	1025	1	BGAL_KLULA

ALIGNMENTS

RESULT 1

ID	OTC_RAT	STANDARD;	PRT;	354 AA.
AC	P00481; Q63407;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ornithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)			
DE	(Otcase) (Ornithine transcarbamylase).			
GN	OTC.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=85063800; PubMed=6095294;			
RA	Takiguchi M., Miura S., Mori M., Tatibana M., Nagata S., Kaziro Y.;			
RT	"Molecular cloning and nucleotide sequence of cDNA for rat ornithine carbamoyltransferase precursor.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:7412-7416(1984).			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Wistar; TISSUE=Liver;			
EX	MEDLINE=87317609; PubMed=3476935;			
RA	Takiguchi M., Murakami T., Miura S., Mori M.;			
RT	"Structure of the rat ornithine carbamoyltransferase gene, a large, x chromosome-linked gene with an atypical promoter.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:6136-6140(1987).			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=85215524; PubMed=3839075;			
RA	Kraus J.P., Hodges P.E., Williamson C.L., Horwich A.L., Kalousek F.,			
RT	Williams K.R., Rosenberg L.E.;			
RT	"A cDNA clone for the precursor of rat mitochondrial ornithine transcarbamylase: comparison of rat and human leader sequences and conservation of catalytic sites.";			
RL	Nucleic Acids Res. 13:943-952(1985).			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=85203360; PubMed=3838931;			
RA	McIntyre P., Graf L., Mercer J.F.B., Wake S.A., Hudson P.J.,			
RT	Hoogenraad N.;			
RT	"The primary structure of the imported mitochondrial protein, ornithine transcarbamylase from rat liver: mRNA levels during ontogeny.";			
RL	DNA 4:147-156(1985).			
RP	SEQUENCE OF 33-56; 293-302; 307-317 AND 321-329.			
RC	TISSUE=Liver;			
EX	MEDLINE=88268748; PubMed=3390141;			
RA	Aoki Y., Sunaga H., Suzuki K.T.;			
RT	"A cadmium-binding protein in rat liver identified as ornithine carbamoyltransferase.";			
RL	Biochem. J. 250:735-742(1988).			
CC	-I- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine - phosphate			

Q8K9g1 buchnera ap
P20740 gallus gall
Q66802 ebola virus
P05733 schizosacch
Q9v122 pyrococcus
O52119 pyrococcus
Q9ug18 homo sapien
P47226 mus musculu
P10581 zea mays (m
P24607 pseudomonas
Q65952 canine aden
Q96685 canine aden

34 47.5 21.9 333 1 Y376_BUCAP
35 47.5 21.9 1473 1 OVOS_CHICK
36 47.5 21.9 2210 1 RRPL_EBOSM
37 47 21.7 90 1 R37B_SCHPO
38 47 21.7 260 1 PSMA_PYPAB
39 47 21.7 260 1 PSMA_PYRHO
40 47 21.7 421 1 TES_HUMAN
41 47 21.7 423 1 TES_MOUSE
42 47 21.7 1098 1 RFOP_MAIZE
43 46.5 21.4 410 1 T801_PSESH
44 46.5 21.4 421 1 VCOM_ADECC
45 46.5 21.4 421 1 VCOM_ADECR

```

CC CC      + L-citrulline.
CC CC      -|- PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
CC CC      -|- SUBUNIT: Homotrimer.
CC CC      -|- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC CC      -|- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC      the European Bioinformatics Institute. There are no restrictions on its
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CC CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC      or send an email to license@isb-sib.ch).
CC CC      -----
CC CC      EMBL: K03040; AAA41768.1; -
CC CC      EMBL: M16933; AAA41769.1; -
CC CC      EMBL: M16924; AAA41769.1; JOINED.
CC CC      EMBL: M16925; AAA41769.1; JOINED.
CC CC      EMBL: M16926; AAA41769.1; JOINED.
CC CC      EMBL: M16928; AAA41769.1; JOINED.
CC CC      EMBL: M16929; AAA41769.1; JOINED.
CC CC      EMBL: M16930; AAA41769.1; JOINED.
CC CC      EMBL: M16932; AAA41769.1; JOINED.
CC CC      EMBL: X01976; CAA26007.1; -
CC CC      EMBL: K00001; AAA41772.1; -
CC CC      EMBL: M11266; AAA41767.1; -
CC CC      PIR: A00563; OWRT.
CC CC      HSP: P00480; 10TH.
CC CC      InterPro: IPR006130; Asp/Orn_Cotranf.
CC CC      InterPro: IPR002292; Orn_carbtransf.
CC CC      InterPro: IPR006131; OTCace_O.
CC CC      InterPro: IPR006132; OTCace_P.
CC CC      Pfam: PF00185; OTCace; 1.
CC CC      Pfam: PF02729; OTCace_N; 1.
CC CC      PRINTS: PR00100; AOTCASE.
CC CC      TIGR: TIGR00658; orni_carb.tr. 1.
CC CC      PROSITE: PS00097; CARBAMOYLTRANSFERASE; 1.
CC CC      Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
CC CC      Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
CC CC      TRANSIT peptide.
CC CC      TRANSIT 1 32 MITOCHONDRION.
CC CC      CHAIN 33 354 ORNITHINE CARBAMOYLTRANSFERASE.
CC CC      ACT_SITE 263 263 BY SIMILARITY.
CC CC      ACT_SITE 303 303 BY SIMILARITY.
CC CC      G -> P (IN REF. 3; AAA41772).
CC CC      G -> S (IN REF. 3).
CC CC      CONFLICT 241 241
CC CC      SEQUENCE 354 AA; 39886 MW; 156B511AF7063F0C CRC64;
CC CC      Query Match 91.7%; Score 199; DB 1; Length 354;
CC CC      Best Local Similarity 97.6%; Pred. No. 9.2e-21;
CC CC      Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC CC      -----
CC CC      Qy 1 MLSNRLILKKAALRKHAHTSMVNFYGRKPVQSQVOLKPRDL 42
CC CC      Dd 1 MLSNRLILKKAALRKHAHTSMVNFYGRKPVQSQVOLKGRDL 42
CC CC      -----
CC CC      RESULT 2
CC CC      OTC_MOUSE STANDARD; PRT; 354 AA.
CC CC      AC P11725;
CC CC      DT 01-OCT-1989 (Rel. 12, Created)
CC CC      DT 01-OCT-1989 (Rel. 12, Last sequence update)
CC CC      DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC CC      DE Ornithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
CC CC      DE (OTCase) (Ornithine transcarbamylase).
CC CC      GN OTC.
CC CC      OS Mus musculus (Mouse).
CC CC      OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC CC      OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC CC      OC NCBI_TaxID=10090;
CC CC      RN [1]
CC CC      RP SEQUENCE FROM N.A.
CC CC      RC STRAIN=C57BL/6J;

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RX MEDLINE=87263407; PubMed=3603027;
RA Veres G., Gibbs R.A., Scherer S.E., Caskey C.T.;
RT "The molecular basis of the sparse fur mouse mutation.";
RL Science 237:415-417(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88157717; PubMed=2831503;
RA Scherer S.E., Veres G., Caskey C.T.;
RT "The genetic structure of mouse ornithine transcarbamylase.";
RL Nucleic Acids Res. 16:1593-1601(1988).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=86224037; PubMed=3011788;
RA Veres G., Craig W.J., Caskey C.T.;
RT "The 5' flanking region of the ornithine transcarbamylase gene
contains DNA sequences regulating tissue-specific expression.";
RL J. Biol. Chem. 261:7588-7591(1986).
CC -|- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
+ L-citrulline.
CC -|- PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
CC -|- SUBUNIT: Homotrimer.
CC -|- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -|- DISEASE: SPARSE FUR (SPF) MOUSE HAVE AN OTC WITH AN OVERALL
DECREASE IN ACTIVITY, AND ALTERED SUBSTRATE AFFINITY.
CC -|- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M17030; AAA39865.1; -
CC EMBL: M1716; AAA39864.1; ALT_SEQ.
CC EMBL: X07092; CAA30121.1; -
CC EMBL: X07093; CAA30121.1; JOINED.
CC EMBL: X07094; CAA30121.1; JOINED.
CC EMBL: X07095; CAA30121.1; JOINED.
CC EMBL: X07096; CAA30121.1; JOINED.
CC EMBL: X07097; CAA30121.1; JOINED.
CC EMBL: X07098; CAA30121.1; JOINED.
CC EMBL: X07099; CAA30121.1; JOINED.
CC EMBL: X07100; CAA30121.1; JOINED.
CC PIR: A43609; OWMS.
CC HSP: P00480; 10TH.
CC SWISS-2DPAGE: P11725; MOUSE.
CC MGD: MGI:97448; Otc.
CC InterPro: IPR006130; Asp/Orn_Cotranf.
CC InterPro: IPR002292; Orn_carbtransf.
CC InterPro: IPR006131; OTCace_O.
CC InterPro: IPR006132; OTCace_P.
CC Pfam: PF00185; OTCace; 1.
CC Pfam: PF02729; OTCace_N; 1.
CC PRINTS: PR00100; AOTCASE.
CC TIGR: TIGR00658; orni_carb.tr. 1.
CC PROSITE: PS00097; CARBAMOYLTRANSFERASE; 1.
CC Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
CC Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
CC TRANSIT peptide.
CC TRANSIT 1 32 MITOCHONDRION.
CC CHAIN 33 354 ORNITHINE CARBAMOYLTRANSFERASE.
CC ACT_SITE 263 263 BY SIMILARITY.
CC ACT_SITE 303 303 BY SIMILARITY.
CC VARIANT 117 117 H -> N (IN SPARSE FUR MOUSE).
CC CONFLICT 195 195 G -> R (IN REF. 2).
CC SEQUENCE 354 AA; 39765 MW; 33BBE5D1E88AA196 CRC64;
CC -----
CC Query Match 75.6%; Score 164; DB 1; Length 354;
CC Best Local Similarity 83.3%; Pred. No. 8.8e-16;
CC Matches 35; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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QY 1 MSLNRLILLNKAALRKAHTSVNRFRYKGPVQSQVQLKPRDL 42
 Db 1 MSLNRLILLNNAALRKGGHTSVRFHWCCKPQSQVQLKGRDL 42

RESULT 3

OTC_HUMAN OTC_HUMAN STANDARD; PRT; 354 AA.
 AC P00480;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ornithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
 DE (OrnCase) (Ornithine transcarbamylase).
 GN OTC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88227905; PubMed=2836378;
 RA Hata A., Tsuzuki T., Shimada K., Takiguchi M., Mori M., Matsuda I.;
 RT "Structure of the human ornithine transcarbamylase gene.";
 RL J. Biochem. 103:302-308(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=84196410; PubMed=6372096;
 RA Horwich A.L., Fenton W.A., Williams K.R., Kalousek F., Kraus J.P.,
 RA Doolittle R.F., Konigsberg W., Rosenberg L.E.;
 RT "Structure and expression of a complementary DNA for the nuclear
 RT coded precursor of human mitochondrial ornithine transcarbamylase.";
 RL Science 224:1068-1074(1984).
 RN [3]
 RP SEQUENCE OF 1-36 FROM N.A.
 RX MEDLINE=85270440; PubMed=3895227;
 RA Horwich A.L., Kalousek F., Rosenberg L.E.;
 RT "Arginine in the leader peptide is required for both import and
 RT proteolytic cleavage of a mitochondrial precursor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4930-4933(1985).
 RN [4]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX MEDLINE=87057134; PubMed=3782067;
 RA Hata A., Tsuzuki T., Shimada K., Takiguchi M., Mori M., Matsuda I.;
 RT "Isolation and characterization of the human ornithine
 RT transcarbamylase gene: structure of the 5'-end region.";
 RL J. Biochem. 100:717-725(1986).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
 RX MEDLINE=99069419; PubMed=9852086;
 RA Shi D., Morizono H., Ha Y., Aoyagi M., Tuchman M., Allewell N.M.;
 RT "1.85-A resolution crystal structure of human ornithine
 RT transcarbamylase complexed with N-phosphonacetyl-L-ornithine.
 RT Catalytic mechanism and correlation with inherited deficiency.";
 RL J. Biol. Chem. 273:34247-34254(1998).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=20274073; PubMed=10813810;
 RA Shi D., Morizono H., Aoyagi M., Tuchman M., Allewell N.M.;
 RT "Crystal structure of human ornithine transcarbamylase complexed with
 RT carbamoyl phosphate and L-norvaline at 1.9 A resolution.";
 RL Proteins 39:271-277(2000).
 RN [7]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=93372868; PubMed=8364586;
 RA Tuchman M.;
 RT "Mutations and polymorphisms in the human ornithine transcarbamylase
 RT gene.";
 RL Hum. Mutat. 2:174-178(1993).
 RN [8]
 RP REVIEW ON VARIANTS.

RX MEDLINE=95353279; PubMed=7627182;
 RA Tuchman M., Plante R.J.;
 RT "Mutations and polymorphisms in the human ornithine transcarbamylase
 RT gene: mutation update addendum.";
 RL Hum. Mutat. 5:293-295(1995).
 RN [9]
 RP REVIEW ON VARIANTS, AND 3D-STRUCTURE MODELING.
 RX MEDLINE=96091868; PubMed=8544185;
 RA Tuchman M., Morizono H., Reish O., Yuan X., Allewell N.M.;
 RT "The molecular basis of ornithine transcarbamylase deficiency:
 RT modelling the human enzyme and the effects of mutations.";
 RL J. Med. Genet. 32:680-688(1995).
 RN [10]
 RP VARIANT OTCD GLN-141.
 RX MEDLINE=89008892; PubMed=3170748;
 RA Maddalena A., Spence J.E., O'Brien W.E., Nussbaum R.L.;
 RT "Characterization of point mutations in the same arginine codon in
 RT three unrelated patients with ornithine transcarbamylase
 RT deficiency.";
 RL J. Clin. Invest. 82:1353-1358(1988).
 RN [11]
 RP VARIANTS OTCD GLN-26; PRO-45 AND GLU-216, AND VARIANT ARG-46.
 RX MEDLINE=89345570; PubMed=2474822;
 RA Grompe M., Muzny D.M., Caskey C.T.;
 RT "Scanning detection of mutations in human ornithine transcarbamylase
 RT by chemical mismatch cleavage.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5888-5892(1989).
 RN [12]
 RP VARIANT OTCD TRP-277.
 RX MEDLINE=90269805; PubMed=2347583;
 RA Finkelstein J.E., Francmano C.A., Brusilow S.W., Travstman M.D.;
 RT "Use of denaturing gradient gel electrophoresis for detection of
 RT mutation and prospective diagnosis in late onset ornithine
 RT transcarbamylase deficiency.";
 RL Genomics 7:167-172(1990).
 RN [13]
 RP VARIANTS OTCD GLN-92 AND LEU-320, AND VARIANT PRO-111.
 RX MEDLINE=91118929; PubMed=1671317;
 RA Grompe M., Caskey C.T., Fenwick R.G. Jr.;
 RT "Improved molecular diagnostics for ornithine transcarbamylase
 RT deficiency.";
 RL Am. J. Hum. Genet. 48:212-222(1991).
 RN [14]
 RP VARIANT OTCD LEU-225.
 RX MEDLINE=92098086; PubMed=1721894;
 RA Hentzen D., Pelet A., Feldman D., Rabier D., Berthelot J.,
 RA Munnich A.;
 RT "Fatal hyperammonemia resulting from a C-to-T mutation at a MspI site
 RT of the ornithine transcarbamylase gene.";
 RL Hum. Genet. 88:153-156(1991).
 RN [15]
 RP VARIANTS OTCD GLU-79; THR-94; PHE-304 AND ASP-345.
 RX MEDLINE=93126062; PubMed=1480464;
 RA Tuchman M., Holzknecht R.A., Gueron A.B., Berry S.A., Tsai M.Y.;
 RT "Six new mutations in the ornithine transcarbamylase gene detected by
 RT single-strand conformational polymorphism.";
 RL Pediatr. Res. 32:600-604(1992).
 RN [16]
 RP SEQUENCE OF 269-289 FROM N.A., AND VARIANT OTCD GLN-277.
 RX MEDLINE=94362689; PubMed=8081373;
 RA Gilbert-Dussardier B., Rabier D., Strautnieks S., Segues B.,
 RA Bonnefont J.-P., Munnich A.;
 RT "A novel arginine (245) to glutamine change in exon 8 of the ornithine
 RT carbamoyl transferase gene in two unrelated children presenting with
 RT late onset deficiency and showing the same enzymatic pattern.";
 RL Hum. Mol. Genet. 3:831-832(1994).
 RN [17]
 RP VARIANT OTCD PRO-140.
 RX MEDLINE=93373296; PubMed=8099056;
 RA Tsai M.Y., Holzknecht R.A., Tuchman M.;
 RT "Single-strand conformational polymorphism and direct sequencing
 RT applied to carrier testing in families with ornithine
 RT transcarbamylase deficiency.";

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RL Hum. Genet. 91:321-325(1993).
RN [18]
RP VARIANTS OTCD LEU-117; LEU-182 AND CYS-203.
RX MEDLINE=94290509; PubMed=8018569;
RA Tuchman M., Pianté R.J., Giguere Y., Lemieux B.;
RT "The ornithine transcarbamylase gene: new 'private' mutations in four
RN patients and study of a polymorphism.";
RL Hum. Mutat. 3:318-320(1994).
RN [19]
RP VARIANTS OTCD GLY-126; HIS-129 AND MET-172.
RX MEDLINE=94362715; PubMed=8081398;
RA Masuura T., Hoshida R., Kiwaki K., Komaki S., Koike E., Endo F.,
RA Oyanagi K., Suzuki Y., Kato I., Ishikawa K., Yoda H., Kamitani S.,
RA Sakaki Y., Matsuda I.;
RT "Four newly identified ornithine transcarbamylase (OTC) mutations
RN (D126G, R129H, I172M and W32X) in Japanese male patients with early-
RN onset OTC deficiency.";
RL Hum. Mutat. 3:402-406(1994).
RN [20]
RP VARIANTS OTCD HIS-40; HIS-129; ARG-195; THR-225; GLN-277 AND
RP GLU-309 DEL.
RX MEDLINE=95038770; PubMed=7951259;
RA Tuchman M., Plante R.J., McCann M.T., Qureshi A.A.;
RT "Seven new mutations in the human ornithine transcarbamylase gene.";
RN Hum. Mutat. 4:57-60(1994).
RN [21]
RP VARIANTS OTCD THR-159 AND VAL-209.
RX MEDLINE=96070988; PubMed=8530002;
RA Garcia-Perez M.A., Sanjurjo P., Briones P., Garcia-Munoz M.J.,
RA Rubio V.;
RT "A splicing mutation, a nonsense mutation (Y167X) and two missense
RN mutations (I159T and A209V) in Spanish patients with ornithine
RN transcarbamylase deficiency.";
RL Hum. Genet. 96:549-551(1995).
RN [22]
RP VARIANTS OTCD GLU-269.
RX MEDLINE=96086561; PubMed=7474905;
RA Zimmer K.P., Matsura T., Colombo J.-P., Koch H.G., Ullrich K.,
RA Deufel T., Harms E., Matsuda I.;
RT "A novel point mutation at codon 269 of the ornithine
RN transcarbamylase (OTC) gene causing neonatal onset of OTC
RN deficiency.";
RL J. Inher. Metab. Dis. 18:356-357(1995).
RN [23]
RP VARIANTS OTCD MET-125; ARG-188; VAL-209 AND LEU-302.
RX MEDLINE=96400964; PubMed=8807340;
RA Gilbert-Dussardier B., Segues B., Rozet J.-M., Rabier D., Calvas P.,
RA de Lunley L., Bonafant J.-P., Munnich A.;
RT "Partial duplication (dup. TCAC (178)) and novel point mutations
RN (T125W, G188R, A209V, and H302L) of the ornithine transcarbamylase
RN gene in congenital hyperammonemia.";
RL Hum. Mutat. 8:74-76(1996).
RN [24]
RP VARIANTS OTCD HIS-40; ASN-88; TYR-202 AND ASN-263.
RA Guardamagna O., Gatti E., Parini R., Plante R.J., Tuchman M.;
RT "Genotype-phenotype correlations in ornithine transcarbamylase
RN deficiency.";
RL Enzyme Protein 49:191-191(1996).
RN [25]
RP VARIANTS OTCD ASN-88; CYS-176; ALA-220; TYR-302 AND LYS-343.
RX MEDLINE=97114289; PubMed=8956038;

Query Match 65.0%; Score 141; DB 1; Length 354;
Best Local Similarity 69.0%; Pred. No. 1.7e-12;
Matches 29; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 MLNRLRLNKAALRAKHAFTSMVRNFRYKPVQSOVOLKPRDL 42
   ||||| ||| | | ||||| | | | | | | | | | | | |
DB 1 MLNRLRLNKAALRAKHAFTSMVRNFRYKPVQSOVOLKPRDL 42

RESULT 4
IF2P_METAC
ID IF2P_METMA STANDARD; PRT; 591 AA.

Query Match 27.2%; Score 59; DB 1; Length 597;
Best Local Similarity 33.3%; Pred. No. 1.4;
Matches 14; Conservative 13; Mismatches 11; Indels 4; Gaps 2;

QY 3 SNLRLLNKAALRAKHAFTSMVRNFRYKPVQSOVOLKPRDL 42
   | | | | | | | | | | | | | | | | | | | | | |
DB 255 ATLQVILYDGLTKKGDVTWIGSL--GEPIQIKVALLKAPREL 294

RESULT 5
IF2P_METMA
ID IF2P_METMA STANDARD; PRT; 591 AA.

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AC Q8PU78;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable translation initiation factor IF-2.
GN INFB OR MM2463.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Brueggemann H., Llenard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
RT transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
CC -!- FUNCTION: Function in general translation initiation by promoting
CC the binding of the formylmethionine-tRNA to ribosomes. Seems to
CC function along with eIF-2 (By similarity).
CC -!- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
CC -----
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CC -----
DR EMBL; A8013490; AAM32159.1; -
DR HAMAP; MF_00100; -
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR000178; IF2.
DR InterPro; IPR005225; Small_GTP.
DR InterPro; IPR004544; TIF_aIF-2.
DR Pfam; PF00009; GTP_EFTU_1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PRINTS; PRO0315; ELONGATNFC.
DR TIGRFAMs; TIGR00491; aIF-2; 1.
DR TIGRFAMs; TIGR00231; Small_GTP; 1.
DR PROSITE; PS01176; IF2; FALSE_NEG.
DR Initiation factor; Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT NP_BIND 16 23 GTP (BY SIMILARITY).
FT NP_BIND 78 82 GTP (BY SIMILARITY).
FT NP_BIND 132 135 GTP (BY SIMILARITY).
SQ SEQUENCE 591 AA; 64900 MW; FE328265BBD887DF CRC64;

Query Match 25.8%; Score 56; DB 1; Length 591;
Best Local Similarity 33.3%; Pred. No. 3.7;
Matches 14; Conservative 13; Mismatches 11; Indels 4; Gaps 2;

QY 3 SNLRILLNKAALRKHAHTSMVRNFRYGKPVQSQVQ--LKPRDL 42
: | | | | | | | | | | | | | | | | | | | | | |
Db 249 ATLIDILYDGTLLKGGTVVIGSL--GEPIRTKVRALLKPREL 288

RESULT 6
OTC_RANCA STANDARD; PRT; 350 AA.
AC P31326;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ornithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
DE (OTCase) (Ornithine transcarbamylase).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93177976; PubMed=1291156;
RA Heibing C., Gergely G., Atkinson B.G.;
RT "Sequential up-regulation of thyroid hormone beta receptor, ornithine
RT transcarbamylase, and carbamyl phosphate synthetase mRNAs in the
RT liver of Rana catesbeiana tadpoles during spontaneous and thyroid
RT hormone-induced metamorphosis.";
RL Dev. Genet. 13:289-301(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Iwase K., Yamauchi K., Ishikawa K.;
RT "Molecular cloning of bullfrog (Rana catesbeiana) ornithine
RT transcarbamylase and induction of its mRNA during spontaneous
RT metamorphosis.";
RL Rep. Fac. Sci. Shizuoka Univ. 29:45-54(1995).
CC -!- FUNCTION: OTC IS NECESSARY FOR THE TADPOLES TRANSITION FROM AN
CC AMMONOTELIC, AQUATIC LARVA TO A UREOTELIC, TERRESTRIAL ADULT.
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
CC + L-citrulline.
CC -!- PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- TISSUE SPECIFICITY: LIVER.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYONIC DEVELOPMENT.
CC -!- INDUCTION: By thyroid hormone.
CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
CC -----
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CC -----
DR EMBL; M95193; AAA49528.1; -
DR EMBL; D38304; BAA22775.1; -
DR PIR; A48421; A48421.
DR HSP; P00480; IOTF.
DR InterPro; IPR006130; Asp/Orn_Cotransf.
DR InterPro; IPR002292; Orn_carbtransf.
DR InterPro; IPR006131; OTCace_O.
DR InterPro; IPR006132; OTCace_P.
DR Pfam; PF00185; OTCace; 1.
DR Pfam; PF02729; OTCace_N; 1.
DR PRINTS; PR00100; AOTCASE.
DR TIGRFAMs; TIGR00658; orn_carb_tr; 1.
DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
DR Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 30 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 31 350 ORNITHINE CARBAMOYLTRANSFERASE.
FT ACT_SITE 259 259 BY SIMILARITY.
FT ACT_SITE 299 299 BY SIMILARITY.
SQ SEQUENCE 350 AA; 39636 MW; EIE598355F03C13E CRC64;

Query Match 25.3%; Score 55; DB 1; Length 350;
Best Local Similarity 38.1%; Pred. No. 2.9;
Matches 16; Conservative 9; Mismatches 13; Indels 4; Gaps 2;

QY 1 MSLNRLILLNKAALRKHAHTSMVRNFRYGKPVQSQVQVQLKPRDL 42
: | | | | | | | | | | | | | | | | | | | | | |
Db 1 MLHMRITIN-ASWRYGNKICVRQFGFS---QTYSQLKGRDL 38

RESULT 7
RR2_LOTJA

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ID AC RR2_LOTJA STANDARD; PRT; 236 AA.
AC O9BS6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S2.
GN RPS2.
OS Lotus japonicus.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Accession MG-20;
RX MEDLINE=21082929; PubMed=11214967;
RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus
  japonicus.";
RL DNA Res. 7:323-330(2000).
CC -1- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC EMBL: AP002983; BAB33197.1;
CC HAMAP: MF_00291;
CC InterPro: IPR001865; Ribosomal_S2.
CC Pfam: PF00318; Ribosomal_S2; 1.
CC PRINTS: PR00395; Ribosomal_S2.
CC PROSITE: PS00962; RIBOSOMAL_S2_1; 1.
CC PROSITE: PS00963; RIBOSOMAL_S2_2; 1.
CC Ribosomal protein; Chloroplast.
CC KW RIBOSOMAL;
CC SEQUENCE 236 AA; 26982 MW; CE92385732325586 CRC64;
CC
CC Query Match 24.9%; Score 54; DB 1; Length 236;
CC Best Local Similarity 38.5%; Pred. No. 2.6;
CC Matches 10; Conservative 10; Mismatches 4; Indels 2; Gaps 1;
CC
QY 2 LSNRLILNKA--ALKRAHTSMVRNF 25
Db 211 IASIRILNKLVAICEGSHSVIRNF 236
      :::::::::::|:::|:::|
RESULT 8
HEMN_SALTY STANDARD; PRT; 457 AA.
ID HEMN_SALTY
AC P37129;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Oxygen-independent coproporphyrinogen III oxidase (EC 1.1.1.17)
DE (Coproporphyrinogenase) (Coprogen oxidase).
GN HEMN OR STM4004 OR SNT3877 OR R3617.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2;
RX MEDLINE=94252986; PubMed=8195073;
RA Xu K., Elliott T.;
RT "Cloning, DNA sequence, and complementation analysis of the

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RT Salmonella typhimurium hemN gene encoding a putative
RT oxygen-independent coproporphyrinogen III oxidase.";
RT J. Bacteriol. 176:3196-3203(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., All J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
  LT2.";
RL Nature 413:852-856(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krohn A., Larsen R.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
  enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
  and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: ANAEROBIC TRANSFORMATION OF COPROPORPHYRINOGEN-III INTO
CC PROTOPORPHYRINOGEN-IX.
CC -1- COFACTOR: REQUIRES MAGNESIUM, ATP AND NAD (OR NADP) FOR ACTIVITY.
CC -1- PATHWAY: Porphyrin biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ANAEROBIC COPROPORPHYRINOGEN III
CC OXIDASE FAMILY.
CC -----
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CC -----
CC EMBL: U06779; AAA19690.1;
CC EMBL: AE008887; AAL22843.1;
CC EMBL: AL627280; CAD03096.1;
CC EMBL: AE016846; AAO71118.1;
CC StyGene: SG10154; hemN
CC InterPro: IPR006638; Eip3.
CC InterPro: IPR004558; hemN.
CC Pfam: PF04055; Radical_SAM; 1.
CC SMART: SM00729; Eip3; 1.
CC TIGRFAMs: TIGR00538; hemN; 1.
CC Porphyrin biosynthesis; Oxidoreductase; Magnesium; NAD;
CC Complete proteome.
CC KW SEQUENCE 457 AA; 52828 MW; 5667B4FE76204DAB CRC64;
CC
CC Query Match 24.9%; Score 54; DB 1; Length 457;
CC Best Local Similarity 26.5%; Pred. No. 5.3;
CC Matches 9; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

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CGS5_YEAST          STANDARD;          PRT;      435 AA.
AC P30283;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-phase entry cyclin 5.
DE CLB5 OR YPR120C OR P9642.8.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BF264-15D;
RX MEDLINE=92387544; PubMed=1387626;
RA Epstein C.B., Cross F.R.
RT "CLB5: a novel B cyclin from budding yeast with a role in S phase.";
RL Genes Dev. 6:1695-1706(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB320;
RX MEDLINE=93307652; PubMed=8319908;
RA Schwob E., Nasmyth K.;
RT "CLB5 and CLB6, a new pair of B cyclins involved in DNA replication
in Saccharomyces cerevisiae.";
RL Genes Dev. 7:1160-1175(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=94074543; PubMed=8253070;
RA Kuehne C., Linder P.;
RT "A new pair of B-type cyclins from Saccharomyces cerevisiae that
function early in the cell cycle.";
RL EMBO J. 12:3437-3447(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=97313271; PubMed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoorge W.,
RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Delius H., Dipaolo T., Dubois E., Duesterhoeft A.,
RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
RA Hunnicke-Smith S., Hyman R., Johnston M., Kaiman S., Kleine K.,
RA Kemp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
RA Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,
RA Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,
RA Urestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
RA Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
RA Zhong W.W., Zollner A., Vo D.H., Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL Nature 387:103-105(1997).
CC -1- FUNCTION: REQUIRED FOR EFFICIENT PROGRESSION THROUGH S PHASE AND
CC POSSIBLY FOR THE NORMAL PROGRESSION THROUGH MEIOSIS. INTERACTS
CC WITH CDC28
CC -1- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED JUST BEFORE CELL CYCLE
CC START.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
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CC -----
DR EMBL; M91209; AAA34503.1; -
DR EMBL; X70435; CAA9893.1; -

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DR EMBL; U40828; AAB68061.1; -
DR PIR; S31290; S31290.
DR SGD; S0006324; CLB5.
DR GO; GO:0000534; C:nucleus; IDA.
DR GO; GO:0000082; P:G1/S transition of mitotic cell cycle; IEP.
DR GO; GO:0000086; P:G2/M transition of mitotic cell cycle; IEP.
DR GO; GO:0006279; P:premeiotic DNA synthesis; IGI.
DR InterPro; IPR006570; Cyclin_Cterm.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Multigene family.
SQ SEQUENCE 435 AA; 50431 MW; 5AD67EB841BA5759 CRC64;

Query Match      24.4%; Score 53; DB 1; Length 435;
Best Local Similarity 46.4%; Pred. No. 7;
Matches 13; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 3 SNLRLLNKALRKAKTSMVNFYQKP 30
   ||||| ||| ||| ||| ||| |||
DB 28 SNLKILQNKRLSRNDSSKQKVQDSKP 55

RESULT 12
EPFL_CHLMU
ID EPFL_CHLMU STANDARD; PRT; 185 AA.
AC Q9PKR6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor P 1 (EF-P 1).
GN EFPL OR TC0398.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- FUNCTION: INVOLVED IN PEPTIDE BOND SYNTHESIS. STIMULATES EFFICIENT
CC TRANSLATION AND PEPTIDE-BOND SYNTHESIS ON NATIVE OR RECONSTITUTED
CC 70S RIBOSOMES IN VITRO. PROBABLY FUNCTIONS INDIRECTLY BY ALTERING
CC THE AFFINITY OF THE RIBOSOME FOR AMINOACYL-TRNA, THUS INCREASING
CC THEIR REACTIVITY AS ACCEPTORS FOR PEPTIDYL TRANSFERASE
CC (BY SIMILARITY).
CC -1- PATHWAY: Protein biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the elongation factor P family.
CC -----
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CC -----
DR EMBL; AE002306; AAF39255.1; -
DR PIR; B81708; B81708.
DR TIGR; TC0398; -
DR HAMAP; MF_00141; -; 1.
DR InterPro; IPR001059; EF-P.

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DR PIR; F85702; DR
DR PIR; G90844; DR
DR PIR; S26137; RGENX.
DR Ecogene; EG10646; narX.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003660; HAMF.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005457; His_kinase.
DR Pfam; PF02518; HAMF; 1.
DR SMART; SM00304; HAMF; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00388; HiskA; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR Sensory transduction; Transferrase; Kinase; Phosphorylation;
KW Transmembrane; Inner membrane; Nitrate assimilation;
KW Complete proteome.
FT DOMAIN 1 14
FT TRANSMEM 15 37
FT DOMAIN 38 151
FT TRANSMEM 152 174
FT DOMAIN 175 588
FT DOMAIN 176 228
FT DOMAIN 393 587
FT MOD_RES 399 399
FT CONFLICT 42 52
FT CONFLICT 374 374 A -> G (IN REF. 7).
FT SEQUENCE 598 AA; 67093 MW; 86GBA0FC2C8F3C3E CRC64;

Query Match 24.0%; Score 52; DB 1; Length 598;
Best Local Similarity 31.0%; Pred. NO. 14;
Matches 13; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

QY 1 MLSNRLINKAAALRKAHTSMVRNF--RYGKPVQSQVLKPR 40
DB 448 LITFLQLTEGLRPALEASCEYSARGFVKLDYLQPPR 489

RESULT 14
POPF SCHPO STANDARD; PRT; 506 AA.
AC Q09855; Q9P7V1;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE F-box/WD-repeat protein pof1l.
GN POF11 OR SPAC29E6.01 OR SPAC30.05.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21668955; PubMed=11809834;
RA Katayama S., Kitamura K., Lehmann A., Nikaido O., Toda T.;
RT "Fission yeast F-box protein Pof3 is required for genome integrity and telomere function.";
RL Mol. Biol. Cell 13:211-224(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne R., Lyne R., Stewart A.,
RA Sgueros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltham T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Buckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA PIR; F85702; Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren I., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe";
RL Nature 415:871-880(2002).
CC 1- SIMILARITY: Contains 1 F-box domain.
CC 1- SIMILARITY: Contains 7 WD repeats.

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EMBL; AB061694; BAB5543.1;
EMBL; AL136538; CAB66464.1;
EMBL; Z66525; CAA91423.1;
PIR; T50211; T50211
GenBank; SPAC29E6.01;
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
Pfam; PF00546; F-box; 1.
Pfam; PF0400; WD40; 7.
PRINTS; PR00320; GPOTEINBRPT.
ProDom; PD000018; WD40; 1.
SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 8.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS_1; 3.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Repeat; WD repeat.
FT DOMAIN 70 116 F-BOX.
FT REPEAT 219 256 WD 1.
FT REPEAT 259 298 WD 2.
FT REPEAT 301 338 WD 3.
FT REPEAT 345 386 WD 4.
FT REPEAT 388 426 WD 5.
FT REPEAT 427 464 WD 6.
FT REPEAT 468 505 WD 7.
SQ SEQUENCE 506 AA; 58257 MW; CEF34D4EFFBC2E10-CRC64;

Query Match 23.5%; Score 51; DB 1; Length 506;
Best Local Similarity 44.4%; Pred. No. 16;
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 3 SNLRILLNKAAALRKAHTSMVRNFYRGK 29
DB 172 SNGRPLLNWSLYKEHAHLDSNRHGR 198

RESULT 15
YK37 YEAST
ID YK37_YEAST STANDARD; PRT; 705 AA.
AC Q03824;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical 81.5 kDa protein in HLJ1-SMP2 intergenic region.
GN YMR163C OR YMR520.12C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Iye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
XIII.";
RL Nature 387:90-93(1997).
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z49705; CAA89799.1; -.
DR PIR: S54521; S54521.
DR SGD: S0004773; YMR163C.
KW Hypothetical protein.
SQ SEQUENCE 705 AA; 81466 MW; E4F2A4D205A98F66 CRC64;

Query Match 23.5%; Score 51; DB 1; Length 705;
Best Local Similarity 36.8%; Pred. No. 23;
Matches 14; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 5 LRTLLNKAALRKHAHTSMVNRFRYGPVQSQVQLKPRDL 42
|| : |||| | | | : | | : | |
Db 643 LRTAKSFELLRKAQASMSVKGFGFKPLRDDAFLESRPL 680

Search completed: July 24, 2003, 22:04:32
Job time : 8.67857 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 24, 2003, 22:02:24 ; Search time 14.3333 Seconds
(without alignments)
288.506 Million cell updates/sec

Title: US-08-765-244-22

Perfect score: 217

Sequence: 1 MLSNRLINKAALRAHIS.....NFRYKPVQSVQLPRDLIC 43

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	199	91.7	354 1	OWRT
2	164	75.6	354 1	OWMS
3	141	65.0	354 1	OWHU
4	119	54.8	41 2	I52779
5	61	28.1	1286	2 E71413
6	60	27.6	351 2	F90409
7	57	26.3	354 2	JE0309
8	55.5	25.6	454 2	A86345
9	55	25.3	350 2	A48421
10	54	24.9	300 2	T32702
11	54	24.9	457 2	AD0950
12	54	24.9	1225 2	A56314
13	53.5	24.7	425 2	I40646
14	53	24.4	435 2	S31290
15	53	24.4	593 2	T47000
16	53	24.4	593 2	AB0239
17	52.5	24.2	185 2	B81708
18	52	24.0	213 2	B83182
19	52	24.0	335 2	T33457
20	52	24.0	598 1	R6ECNX
21	52	24.0	598 2	F85702
22	52	24.0	598 2	G90844
23	51.5	23.7	260 2	G70233
24	51	23.5	506 2	T50211
25	51	23.5	598 2	AF0648
26	51	23.5	633 2	S76749
27	51	23.5	705 2	S54521
28	51	23.5	1779 2	T23130
29	50.5	23.3	138 2	F81900

30 50.5 23.3 383 2 B83922 short-chain-specif
31 50.5 23.3 429 2 E90267 hypothetical prote
32 50 23.0 178 2 F91180 hypothetical prote
33 50 23.0 178 2 H86026 hypothetical prote
34 50 23.0 202 2 F40590 mo:B homolog lafu
35 50 23.0 338 2 H75127 CAAX prenyl protei
36 50 23.0 386 2 F72773 probable molybdopt
37 50 23.0 616 2 A58947 signal recognition
38 50 23.0 662 2 AB1979 calcium-dependent
39 49.5 22.8 467 2 G83266 cytochrome c PA303
40 49.5 22.8 864 2 B90395 purine NPase [imp
41 49.5 22.8 1164 2 T03814 tumor suppressor p
42 49 22.6 176 2 S57240 18c protein (clone
43 49 22.6 301 2 T33068 hypothetical prote
44 49 22.6 353 1 B69518 GTP-binding protei
45 49 22.6 446 2 C81719 conserved hypothet

ALIGNMENTS

RESULT 1

OWRT
ornithine carbamoyltransferase (EC 2.1.3.3) precursor - rat
N:Alternate names: citrulline phosphorylase; ornithine transcarbamylase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1986 #sequence revision 28-Feb-1986 #text change 11-Jun-1999
C:Accession: A00563; A28042; A23090; S02466; I52976; I67609; I53457
R:Rakiguchi, M.; Miura, S.; Mori, M.; Tatibana, M.; Nagata, S.; Kaziro, Y.
Proc. Natl. Acad. Sci. U.S.A. 81, 7412-7416, 1984
A:Title: Molecular cloning and nucleotide sequence of cDNA for rat ornithine carbamoyltransferase
A:Reference number: A00563; MUID:85063800; PMID:6095294
A:Accession: A00563
A:Molecule type: mRNA
A:Residues: 1-354 <TAK1>
A:Cross-references: GB:K03040; NID:9205873; PIDN:AAA41768.1; PID:9205874
R:Rakiguchi, M.; Murakami, T.; Miura, S.; Mori, M.
Proc. Natl. Acad. Sci. U.S.A. 84, 6136-6140, 1987
A:Title: Structure of the rat ornithine carbamoyltransferase gene, a large, X chromo:
A:Reference number: A28042; MUID:87317609; PMID:3476935
A:Accession: A28042
A:Molecule type: DNA
A:Residues: 1-354 <TAK2>
A:Cross-references: GB:M16933; GB:J02957; NID:9205884; PIDN:AAA41769.1; PID:9205886
R:Kraus, J.P.; Hodges, P.E.; Williamson, C.L.; Horwich, A.L.; Kalousek, F.; Williams, Nucleic Acids Res. 13, 943-952, 1985
A:Title: A cDNA clone for the precursor of rat mitochondrial ornithine transcarbamylase
A:Reference number: A23090; MUID:85215524; PMID:3839075
A:Accession: A23090
A:Molecule type: mRNA
A:Residues: 1-38, 'P', 40-240, 'S', 242-354 <KRA>
A:Cross-references: GB:X01976
R:Aoki, Y.; Sunaga, H.; Suzuki, K.T.
Biochem. J. 250, 735-742, 1988
A:Title: A cadmium-binding protein in rat liver identified as ornithine carbamoyltransferase
A:Reference number: S02466; MUID:88268748; PMID:3390141
A:Accession: S02466
A:Molecule type: protein
A:Residues: 33-56;293-302;307-317;322-329 <AOK>
R:McIntyre, P.; Graf, L.; Mercer, J.F.B.; Wake, S.A.; Hudson, P.J.; Hoogenraad, N. DNA 4, 147-156, 1985
A:Title: The primary structure of the imported mitochondrial protein, ornithine transcarbamoyltransferase
A:Reference number: I52976; MUID:85203360; PMID:3838931
A:Accession: I52976
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>
A:Cross-references: GB:M1266; NID:9205871; PIDN:AAA41767.1; PID:9205872
R:McIntyre, P.; Graf, L.; Mercer, J.; Peterson, G.; Hudson, P.J.; Hoogenraad, N. FEBS Lett. 177, 41-46, 1984
A:Title: A highly basic N-terminal extension of the mitochondrial matrix enzyme ornithine carbamoyltransferase
A:Reference number: I53457; MUID:85051832; PMID:6548714
A:Accession: I67609

A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-102 <RE2>
 A:Cross-references: EMBL:X01178; NID:g56802; PIDN:CAA25618.1; PID:g56803
 A:Accession: I53457
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-43, 'N', 45-99, 'R', 101-102 <RE3>
 A:Cross-references: GB:K03041; NID:g205889; PIDN:AAA41771.1; PID:g205890
 C:Genetics:
 A:Introns: 26/2; 72/3; 100/1; 129/2; 180/3; 221/3; 239/3; 289/3; 335/3
 C:Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
 C:Keywords: arginine biosynthesis; homotrimer; mitochondrion; transferase; urea cycle
 F:1-32/Domain: transit peptide (mitochondrion) #status predicted <TNP>
 F:33-354/Product: ornithine carbamoyltransferase #status predicted <NAT>
 F:40-342/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>

Query Match 91.7%; Score 199; DB 1; Length 354;
 Best Local Similarity 97.6%; Pred. No. 9.3e-20;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLSNRLILLNKAALRKHAHTSMVRNFRYKPKVQSQVQLKPRDL 42
 DB 1 MLSNRLILLNKAALRKHAHTSMVRNFRYKPKVQSQVQLKGRDL 42

RESULT 2

OWHU

ornithine carbamoyltransferase (EC 2.1.3.3) precursor - mouse
 N:Alternate names: citrulline phosphorylase; ornithine transcarbamylase
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Mar-1993 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999
 C:Accession: A43609; S03407; I55252
 R:Veres, G.; Gibbs, R.A.; Scherer, S.E.; Caskey, C.T.
 Science 237, 415-417, 1987
 A:Title: The molecular basis of the sparse fur mouse mutation.
 A:Reference number: A43609; MUID:87263407; PMID:3603027
 A:Accession: A43609
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-354 <VER>
 A:Cross-references: GB:ML7030; NID:g200162; PIDN:AAA39865.1; PID:g200163
 R:Scherer, S.E.; Veres, G.; Caskey, C.T.
 Nucleic Acids Res. 16, 1593-1601, 1988
 A:Title: The genetic structure of mouse ornithine transcarbamylase.
 A:Reference number: S03407; MUID:88157177; PMID:2831503
 A:Accession: S03407
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-194, 'R', 196-335 <SCH>
 A:Cross-references: EMBL:X07092
 R:Veres, G.; Craigen, W.J.; Caskey, C.T.
 J. Biol. Chem. 261, 7588-7591, 1986
 A:Title: The 5' flanking region of the ornithine transcarbamylase gene contains DNA sequence information for the mouse ornithine transcarbamylase.
 A:Reference number: I55252; MUID:86224037; PMID:3011788
 A:Accession: I55252
 A:Status: translation not shown; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-19, 'LLWFDF', <RES>
 A:Cross-references: GB:ML2176; NID:g200160; PIDN:AAA39864.1; PID:g554248
 A:Note: the end of this sequence is near the boundary of the cloned region and may be an artifact.
 C:Genetics:
 A:Gene: OTC

A:Map position: X
 A:Introns: 26/2; 72/3; 100/1; 129/2; 180/3; 221/3; 239/3; 289/3
 C:Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
 C:Keywords: mitochondrion; transferase; urea cycle
 F:1-32/Domain: transit peptide (mitochondrion) #status predicted <TNP>
 F:33-335/Product: ornithine carbamoyltransferase #status predicted <NAT>
 F:40-342/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>
 Query Match 75.6%; Score 164; DB 1; Length 354;
 Best Local Similarity 83.3%; Pred. No. 6.6e-15;

Matches 35; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MLSNRLILLNKAALRKHAHTSMVRNFRYKPKVQSQVQLKPRDL 42
 DB 1 MLSNRLILLNKAALRKHAHTSMVRNFRYKPKVQSQVQLKGRDL 42
 RESULT 3
 OWHU
 ornithine carbamoyltransferase (EC 2.1.3.3) precursor - human
 N:Alternate names: citrulline phosphorylase; ornithine transcarbamylase
 C:Species: Homo sapiens (man)
 C>Date: 28-Feb-1986 #sequence_revision 31-Mar-1993 #text_change 16-Jun-2000
 C:Accession: B41444; A00562; I38078; JC4672; I59039; I54377
 R:Hata, A.; Tsuzuki, T.; Shimada, K.; Takiguchi, M.; Mori, M.; Matsuda, I.
 J. Biochem. 103, 302-308, 1988
 A:Title: Structure of the human ornithine transcarbamylase gene.
 A:Reference number: A41444; MUID:88227905; PMID:2836378
 A:Accession: A41444
 A:Molecule type: DNA
 A:Residues: 1-354 <HAT>
 A:Cross-references: GB:D00230; NID:g219957; PIDN:BAA00161.1; PID:g219959
 A:Accession: B41444
 A:Molecule type: mRNA
 A:Residues: 1-354 <HA2>
 A:Cross-references: GB:D00230; NID:g219957; PIDN:BAA00161.1; PID:g219959
 R:Horwich, A.L.; Fenton, W.A.; Williams, K.R.; Kalousek, F.; Kraus, J.P.; Doolittle, R.
 Science 224, 1068-1074, 1984
 A:Title: Structure and expression of a complementary DNA for the nuclear coded precursor of ornithine carbamoyltransferase.
 A:Reference number: A00562; MUID:84196410; PMID:6372096
 A:Accession: A00562
 A:Molecule type: mRNA
 A:Residues: 1-100, 'F', 102-110, 'P', 112-192, 'CF', 195-269, 'R', 271-354 <HOR>
 A:Cross-references: GB:D00230
 R:Hata, A.; Tsuzuki, T.; Shimada, K.; Takiguchi, M.; Mori, M.; Matsuda, I.
 J. Biochem. 100, 717-725, 1986
 A:Title: Isolation and characterization of the human ornithine transcarbamylase gene.
 A:Reference number: I38078; MUID:87057134; PMID:3782067
 A:Accession: I38078
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-26 <RES>
 A:Cross-references: EMBL:X04443; NID:g35162; PIDN:CAA28039.1; PID:g35163
 R:Wheeler, V.C.; Prodromou, C.P.; Pearl, L.H.; Williamson, R.; Coutelle, C.
 Gene 169, 251-255, 1996
 A:Title: Synthesis of a modified gene encoding human ornithine transcarbamylase for eukaryotic expression.
 A:Reference number: JC4672; MUID:96194812; PMID:8647457
 A:Accession: JC4672
 A:Molecule type: DNA
 A:Residues: 'M', 33-100, 'F', 102-110, 'P', 112-192, 'CF', 195-269, 'R', 271-354 <WHE>
 A:Note: this report represents a synthetic gene designed for expression in (rather than in a cell).
 R:Horwich, A.L.; Kalousek, F.; Rosenberg, L.E.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4930-4933, 1985
 A:Title: Arginine in the leader peptide is required for both import and proteolytic cleavage of the human ornithine transcarbamylase.
 A:Reference number: I59039; MUID:85270440; PMID:3895227
 A:Accession: I59039
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-36 <RE2>
 A:Cross-references: GB:ML1235; NID:g189408; PIDN:AAA59976.1; PID:g189409
 R:Gilbert-Dussardier, B.; Rabier, D.; Strautnieks, S.; Segues, B.; Bonnefont, J.P.; M. Hum. Mol. Genet. 3, 831-832, 1994
 A:Title: A novel arginine (245) to glutamine change in exon 8 of the ornithine carbamoyltransferase gene.
 A:Reference number: I54377; MUID:94362689; PMID:8081373
 A:Accession: I54377
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 269-276, 'Q', 278-289 <RE3>
 A:Cross-references: GB:S73640; NID:g688001; PIDN:AAB31859.1; PID:g688002
 A:Note: this sequence represents a disease defect in ornithine carbamoyltransferase. The active enzyme is a dimer of identical chains with one tightly bound z

Best Local similarity 38.2%; Pred. No. 5.2;
Matches 13; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 3 SNLRILLNKAALKAHTSMVRNFRYGKPVQSOVQ 36
DB 107 SNLRRLSSSTTKRDESLVRNLLVSPQLDQ 140

RESULT 6
F90409
GTP binding conserved hypothetical protein SSO2385 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: F90409
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Cf. Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A98139
A:Accession: F90409
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-351 <KUR>
A:Cross-references: GB:AE006641; NID:gl3815687; PIDN:AAK42533.1; GSPDB:GNO0155
C:Genetics:
A:Gene: SSO2385

Query Match 27.6%; Score 60; DB 2; Length 351;
Best Local Similarity 34.6%; Pred. No. 1.7;
Matches 18; Conservative 8; Mismatches 10; Indels 16; Gaps 3;

QY 7 ILLNKA-----LRKAHTSMVRNFRY---GKPVQSOVQ-----LKPRDL 42
DB 294 LILKGGSTVLDVARKUHLSSLAENFRYARVWGRSVKFGQKGVPSHILEDRI 345

RESULT 7
JE0309
ornithine carbamoyltransferase (EC 2.1.3.3) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jan-2000
C:Accession: JE0309
R;Shimogiri, T.; Kono, M.; Mannen, H.; Mizutani, M.; Tsuji, S.
J. Biochem. 124, 962-971, 1998
A:Title: Chicken ornithine transcarbamylase gene, structure, regulation, and chromosomal reference number: JE0309; MUID:99011321; PMID:9792920
A:Reference number: JE0309
A:Accession: JE0309
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <SHI>
A:Cross-references: GB:AF065629; NID:g4218928; PIDN:AAI2234.1; PID:g4218929
C:Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
C:Keywords: transferase
F:40-342/Domain: aspartate/ornithine carbamoyltransferase homology <AOC>

Query Match 26.3%; Score 57; DB 2; Length 354;
Best Local Similarity 40.5%; Pred. No. 4.5;
Matches 17; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 MLNLRILLNKAALKAHTSMVRNFRYGKPVQSOVQLKPRDL 42
DB 1 MLFNKALNLYRIKLTQNSKHLPRHFCRGPPNQMNWCLKGRDL 42

RESULT 8
A86345
F16F4.13 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C:Accession: A86345
R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

C:Genetics:
A:Gene: CESP:C14C6.13
A:Map position: 5
A:Introns: 9/1; 129/2; 145/3; 267/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C14C6.13

Query Match 24.9%; Score 54; DB 2; Length 300;
Best Local Similarity 31.4%; Pred. No. 9,9;
Matches 11; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 2 LSNRLILLKKAALRKHAHTSMVNRFRYGKPVQSQQV 36
| | | : | : | : | : | : | : | : | : | : |
Db 199 LDNIRELCQSALOKCSETRDPTGTFRYPINIEIQ 233

RESULT 11
AD0950
oxygen-independent coproporphyrinogen III oxidase [imported] - Salmonella enterica ssp.
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
R:Accession: AD0950
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fair
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parky, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A.; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AD0950
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-457 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03095.1; PID:gl6504733; GSPDB:GN00176
C:Genetics:
A:Gene: STY3877
C:Superfamily: oxygen-independent coproporphyrinogen oxidase

Query Match 24.9%; Score 54; DB 2; Length 457;
Best Local Similarity 26.5%; Pred. No. 16;
Matches 9; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 9 LNKAALKRAHTSMVNRFRYGKPVQSQQVLKPRDL 42
| | | : | : | : | : | : | : | : | : | : |
Db 118 LNKAKISRLMTLLRENFHFNTDAEISIEVDPREI 151

RESULT 12
A56514
chromokinesin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 02-Feb-2001
C:Accession: A56514; I50691
R:Wang, S.Z.; Adler, R.
J. Cell Biol. 128, 761-768, 1995
A:Title: Chromokinesin: a DNA-binding, kinesin-like nuclear protein.
A:Reference number: A56514; MUID:95181533; PMID:7876303
A:Accession: A56514
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1225 <WAN>
A:Cross-references: GB:U18309; NID:g603760; PIDN:AAC59666.1; PID:g603761
R:Wang, S.Z.; Adler, R.
Proc. Natl. Acad. Sci. U.S.A. 91, 1351-1355, 1994
A:Title: A developmentally regulated basic-leucine zipper-like gene and its expressio
A:Reference number: A53451; MUID:94151328; PMID:8108415
A:Accession: I50691
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 728-1086, 'RI' <WA2>
A:Cross-references: EMBL:U04821; NID:g440792; PIDN:AAA18960.1; PID:g440793
C:Genetics:
A:Gene: sw3-3

C:Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology
C:Keywords: ATP; DNA binding; mitosis; nucleotide binding; P-loop
F:11-344/Domain: kinesin motor domain homology <KWOT>
F:88-95/Region: nucleotide-binding motif A (P-loop)

Query Match 24.9%; Score 54; DB 2; Length 1225;

Best Local Similarity 39.9%; Pred. No. 46;
Matches 17; Conservative 9; Mismatches 15; Indels 2; Gaps 2;

Qy 2 LSNLRILLNKA-ALRKA-HFSVMRNFYRGKPVQSQVQLKPRDL 42

Db 528 MSKELVELNKAALKEALAKMKIQNDQSLEPIQSQVQTNKDL 570

RESULT 13

I40646

sensor-like protein - Coxiella burnetii

C:Species: Coxiella burnetii

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 31-Mar-2000

C:Accession: I40646

R:Mo, Y.Y.; Mallavia, L.P.

Gene 151, 185-190, 1994

A:Title: A coxiella burnetii gene encodes a sensor-like protein..

A:Reference number: I40646; MUID:95129857; PMID:7828872

A:Accession: I40646

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-425 <RSS>

A:Cross-references: EMBL:U07186; NID:g460628; PIDN:AAA81939.1; PID:g460629

C:Genetics:

A:Gene: gsaA

C:Superfamily: envZ protein; sensor histidine kinase homology

C:Keywords: autophosphorylation; phosphohistidine; phosphoprotein

F:196-421/Domain: sensor histidine kinase homology <SHK>

F:727/Binding site: phosphate (His) (covalent) (by autophosphorylation) #status predicted

Query Match 24.7%; Score 53.5; DB 2; Length 425;

Best Local Similarity 36.4%; Pred. No. 17;

Matches 12; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

Qy 5 LRILLNKAALRKAHTSMVRN-FRYGKPVQSQV 36

Db 311 IKILGRASAKRAFTNLLNNAIRYAKNVNRIQ 343

RESULT 14

S31290

cyclin B5 - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein P9642.8; protein YPR120c

C:Species: Saccharomyces cerevisiae

C:Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 19-Apr-2002

C:Accession: S31290; S36228; S69013

R:Epstein, C.B.; Cross, F.R.

Genes Dev. 6, 1695-1706, 1992

A:Title: CLB5: a novel B cyclin from budding yeast with a role in S phase.

A:Reference number: S31290; MUID:92387544; PMID:1387626

A:Accession: S31290

A:Molecule type: DNA

A:Residues: 1-435 <EPS>

A:Cross-references: EMBL:M91209; NID:g171238; PIDN:AAA34503.1; PID:g171239

R:Schwab, E.; Nasmyth, K.

Genes Dev. 7, 1160-1175, 1993

A:Title: CLB5 and CLB6, a new pair of B cyclins involved in DNA replication in Saccharom

A:Reference number: S36228; MUID:93307652; PMID:8319908

A:Accession: S36228

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-435 <SCH>

A:Cross-references: EMBL:X70435; NID:g396496; PIDN:CAA49893.1; PID:g396497

R:Johnson, D.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of S. cerevisiae cosmid 9642.

A:Reference number: S69014

A:Accession: S69013
A:Molecule type: DNA
A:Residues: 1-435 <JOH>
A:Cross-references: EMBL:U40828; NID:g1066467; PIDN:AAB68061.1; PID:g1066475; MIPS:Y1
C:Genetics:
A:Gene: SGD:CLB5; CLB5
A:Cross-references: SGD:S0006324
A:Map position: 16R
C:Superfamily: cyclin
C:Keywords: cell cycle control

Query Match 24.4%; Score 53; DB 2; Length 435;

Best Local Similarity 46.4%; Pred. No. 20;

Matches 13; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 3 SNLRILLNKAALRKAHTSMVRNFYRGK 30

Db 28 SNLKTIQNKRALSKNDSSSKQVQVDSKP 55

RESULT 15

T47000

nitrate/nitrite sensor protein (EC 2.7.3.-) [similarity] - Yersinia pestis

C:Species: Yersinia pestis

C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000

C:Accession: T47000

R:Buchrieser, C.; Rusniok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; Carr

submitted to the EMBL Data Library, October 1998

A:Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.

A:Reference number: Z24348

A:Accession: T47000

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-593 <RUC>

A:Cross-references: EMBL:AL031866; PIDN:CAA21343.1

A:Experimental source: strain 6/69

C:Superfamily: nitrate/nitrite sensor protein narX

C:Keywords: autophosphorylation; phosphohistidine; phosphoprotein; phosphotransferase

F:401/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 24.4%; Score 53; DB 2; Length 593;

Best Local Similarity 34.1%; Pred. No. 29;

Matches 14; Conservative 8; Mismatches 17; Indels 2; Gaps 1;

Qy 1 MSLNLRILLNKAALRKAHTSMVRNF--RYGKPVQSQVQLKP 39

Db 450 LLFTFRLLKLNLEATLEALQALVNEFSERAGLSITEKYQLPP 490

Search completed: July 24, 2003, 22:08:08

Job time : 16.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 24, 2003, 21:59:18 ; Search time 37.881 Seconds
(without alignments)
180.176 Million cell updates/sec

Title: US-08-765-244-22
Perfect score: 217
Sequence: 1 MSLNLRILLKALRKAKHTS.....NFRYCKPVQSVQLKPRDLIC 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217	100.0	43	17	AA90584
2	159	73.3	32	23	ABG30857
3	109	50.2	258	21	AA18445
4	108	49.8	32	23	ABG30856
5	105	48.4	32	22	RAG64224
6	92	42.4	32	15	AA48260
7	92	42.4	32	20	AAW6358
8	92	42.4	32	23	ABG92993
9	92	42.4	32	24	ABP56588

10	79.5	36.6	31	21	AA15704	Mitochondrial matr
11	79.5	36.6	31	21	AA22835	Mitochondrial matr
12	56.5	26.0	149	22	AAU23468	Novel human enzyme
13	54	24.9	866	22	AB57741	Drosophila melanog
14	53.5	24.7	755	22	AB59259	Drosophila melanog
15	52	24.0	165	20	AAU04933	Mycobacterium spec
16	52	24.0	774	22	ABG29304	Novel human diago
17	52	24.0	1124	22	AB59241	Drosophila melanog
18	51.5	23.7	138	21	AA75465	Neisseria meningit
19	51	23.5	1169	17	AA96126	Bacillus thuringie
20	50.5	23.3	138	21	AA75466	Neisseria meningit
21	50.5	23.3	296	22	AB64170	Drosophila melanog
22	50.5	23.3	2379	23	ABP62760	S. roseosporus dap
23	50	23.0	564	23	ABP73265	Candida albicans e
24	50	23.0	746	22	AA893938	Human protein sequ
25	50	23.0	975	22	AA94042	Human protein sequ
26	50	23.0	975	23	AA018173	Human hydrogen per
27	49	22.6	74	22	AA60044	Propionibacterium
28	49	22.6	457	16	AA78184	E.coli cell divisi
29	49	22.6	624	23	ABR98858	A. niger tripeptid
30	48.5	22.4	75	22	AA64583	Human brain expres
31	48.5	22.4	75	22	AA64583	Peptide #11570 enc
32	48.5	22.4	75	23	ABG46393	Human peptide enco
33	48.5	22.4	185	20	AA737084	Protein involved i
34	48.5	22.4	285	22	AAU33373	Enterococcus faeca
35	48.5	22.4	334	22	AAU35205	Enterococcus faeca
36	48.5	22.4	684	22	AA89868	C. glutamicum prote
37	48.5	22.4	4987	12	AA07559	Protein encoded by
38	48.5	22.4	4987	12	AA07559	Rianodin receptor.
39	48.5	22.4	5035	13	AA25450	MH mutant porcine
40	48.5	22.4	5072	12	AA11510	Ryanodine receptor
41	48.5	22.4	5081	22	ABG04969	Novel human diago
42	48.5	22.4	5081	22	AB11480	Human ryanodine re
43	48	22.1	13	21	AA57007	Peptide MS-34, wit
44	48	22.1	93	22	AB10986	Human transferrin
45	48	22.1	96	21	AA603218	Human secreted pro

ALIGNMENTS

RESULT 1
AA90584
ID AA90584 standard; Protein; 43 AA.
XX
AC AA90584;
XX
DT 25-MAR-2003 (updated)
DE 31-OCT-1996 (first entry)
XX
DE Rat ornithine transcarbamylase signal peptide.
XX
KW promoter; peptide-nucleic acid; cyclised; gene therapy; target;
KW site-directed mutagenesis; introduction; protein transport.
XX
OS Synthetic.
XX
PN DE19520815-AA1.
XX
PD 21-DEC-1995.
XX
PF 11-JUN-1995; 95DE-1020815.
XX
PR 16-JUN-1994; 94DE-4421079.
XX
XX (SEIB/) SEIBEL P.
PI Seibel A, Seibel P;
XX
DR WPI; 1996-041226/05.
XX
PT Replicable and transcriptionally active plasmid carrying signal
PT peptide for specific target - useful for site directed mutagenesis

PT and molecular therapy of genetic diseases.
 XX Disclosure; Column 11; 24pp; German.
 CC
 CC Two modified oligonucleotides (introducing PstI and XhoI sites) were
 CC used to amplify a region of the human mitochondrial (mt) genome contg.
 CC the light strand promoter, mtDNA ori of the heavy strand, CSP/s
 CC ("conserved sequence blocks"), and a regulation site for DNA replication.
 CC Behind this fragment (5' direction) a synthetic multiple cloning site
 CC was introduced, generating a product with overhang ends. The synthetic
 CC region also introduced a bidirectional mt transcription termination
 CC sequence. The amplification product, synthetic fragment and pBluescript
 CC were ligated and recombinant plasmid 1 (AAR12315) was produced. Human mt
 CC 16S rRNA (differing from the native RNA only in having a modified
 CC nucleotide) was isolated by PCR from chloramphenicol resistant HeLa
 CC cells and inserted into plasmid 1 to form plasmid 2 (AAR12316). The
 CC cloned insert was isolated as a BstI fragment and cyclised using hairpin
 CC loop oligonucleotides, one of which carried the required signal peptide
 CC (the present sequence). The cyclised product was purified by treatment
 CC with exonuclease III. In a modification, the signal peptide was attached
 CC after cyclisation. The new plasmids were able to impart chloramphenicol
 CC resistance to otherwise sensitive B lymphocytes and fibroblasts.
 CC Similar plasmids without a signal peptide could not do this. The
 CC plasmids can be introduced into eukaryotic cells, esp. for site-directed
 CC mutagenesis or molecular therapy of genetic diseases, targeting nucleic
 CC acid in cells or their organelles via the protein transport route.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 XX Sequence 43 AA;
 SQ
 Query Match 100.0%; Score 217; DB 17; Length 43;
 Best Local Similarity 100.0%; Pred. No. 3.1e-26;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSNRLILLNKAALRKAHSMVRNFRYKPGVQSVQVKPRDLC 43
 Db 1 MLSNRLILLNKAALRKAHSMVRNFRYKPGVQSVQVKPRDLC 43
 RESULT 2
 ABG30857
 ID ABG30857 standard; Peptide; 32 AA.
 AC ABG30857;
 XX
 XX
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Rat ornithine transcarbamylase signal peptide.
 XX
 XX Rat; signal peptide; ornithine transcarbamylase; MOT;
 KW recombinant vector; fusion protein; extranuclear gene.
 XX
 XX Rattus sp.
 OS
 XX JP2002176988-A.
 PN
 XX
 XX 25-JUN-2002.
 XX
 XX 14-DEC-2000; 2000JP-0380975.
 XX
 XX 14-DEC-2000; 2000JP-0380975.
 PR
 XX (TANAKA/) TANAKA M.
 PA (GIFU-) ZH GIFUKEN KOKUSAI BIO KENYUJO.
 PA (OYOS-) ZH OYO SEIKAGAKU KENYUSHO.
 XX
 XX WPI; 2002-569946/61.
 DR N-PSDB; ABK68419.
 XX
 XX A recombinant vector for expressing a fused protein, useful for
 PT decomposing an extranuclear gene of a nonhuman organism -
 XX Disclosure; Page 3; 15pp; Japanese.
 PS

XX The invention relates to a recombinant vector for expressing a fused
 CC protein containing a fused gene in which a base sequence defining a
 CC transfer signal peptide to small cellular organs having an extranuclear
 CC gene is combined with a base sequence defining the amino acid sequence of
 CC a restriction enzyme recognising a defined base sequence. The vector is
 CC used for decomposing an extranuclear gene of a nonhuman organism.
 CC The present sequence represents the signal peptide of rat mitochondrial
 CC ornithine transcarbamylase (MOT) which may be used in the vector of the
 CC invention.
 XX
 XX Sequence 32 AA;
 SQ
 Query Match 73.3%; Score 159; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.4e-17;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSNRLILLNKAALRKAHSMVRNFRYKPGVQ 32
 Db 1 MLSNRLILLNKAALRKAHSMVRNFRYKPGVQ 32
 RESULT 3
 AAB18445
 ID AAB18445 standard; Protein; 258 AA.
 XX
 XX AC AAB18445;
 XX
 XX DT 15-JAN-2001 (first entry)
 DT
 DE Protein encoded by plasmid pUOATP2.
 XX
 XX Mitochondrial genome; mitochondrial encephalomyopathy; lactic acidosis;
 KW Leber hereditary optic neuropathy; myoclonic epilepsy;
 KW neurogenic muscular weakness; ataxia; retinitis pigmentosa;
 KW Kearns-Sayre syndrome; Leigh syndrome; Pearson Marrow pancreas syndrome;
 KW amnoglycoside-associated deafness; diabetes; deafness; leukodystrophy;
 KW hypotonia; autism; sudden infant death syndrome; hypoglycemia; leukaemia;
 KW thrombocytopenia; migraine; hearing loss; stroke;
 KW refractory infantile reflux; carnitine deficiency; multiple sclerosis;
 KW blindness; optic atrophy; renal tubular acidosis; cardiomyopathy;
 KW chronic pancreatitis; ATPase 6.
 XX
 XX Synthetic.
 OS
 XX WO200053773-A2.
 PN
 XX 14-SEP-2000.
 PD
 XX 08-MAR-2000; 2000WO-US06037.
 PF
 XX 08-MAR-1999; 99US-0123336.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Zullo SJ, Eisenstadt JM;
 PI
 XX WPI; 2000-565602/52.
 DR N-PSDB; AAA75084.
 XX
 XX Functionally complementing one or more defects, mutations, or deletions
 PT in a mitochondrial genome of a cell, useful for treating diabetes with
 PT deafness, comprises introducing mitochondrial DNA into the nuclear
 PT genome -
 XX
 XX Example 1; Fig 3; 49pp; English.
 PS
 CC The specification describes a method for functionally complementing
 CC one or more defects, mutations, or deletions in a mitochondrial genome of
 CC a cell having a nuclear genome. The method is used for treating a disease
 CC or disorder that arises from deletion of the protein-encoding genes of
 CC the mitochondrial genome. Alternatively, the method is used for treating
 CC a disease or disorder that arises from one or more defects, deletions or

ID	AAF48260	standard; peptide; 32 AA.
XX		
XX	AAF48260;	
AC		
XX		
XX		
DT	25-MAR-2003	(updated)
DT	29-JUL-1994	(first entry)

```

XX DE Mitochondrial matrix retention signal.
XX OS
XX FH Single chain antibody; sFv; heavy chain; light chain;
XX KW variable domain; hydrophilic linker; antibodies; targeting;
XX KW subcellular localisation signal; mitochondrial matrix;
XX KW retention signal.
XX OS
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 7 /note= "not defined"
XX FT Misc-difference 8 /note= "not defined"
XX FT Misc-difference 32 /note= "not defined"
XX FT
XX PN WO9402610-A1.
XX PD 03-FEB-1994.
XX PF 16-JUL-1993; 93WO-US06735.
XX PR 17-JUL-1992; 92US-0916939.
XX PR 17-MAR-1993; 93US-0045274.
XX PA (DAND ) DANA FARBER CANCER INST INC.
XX PI Haseltine WA, Marasco WA;
XX XX WPI; 1994-048868/06.
XX XX Intracellular binding of antigens - by using antibody targeting
XX PT with vector system, for e.g. tumour suppression
XX PS
XX PS Disclosure; Page 103; 155pp; English.
XX CC New vector systems comprise a sequence adapted for intracellular
XX CC delivery and expression contg. a promoter operably linked to an
XX CC antibody gene encoding an antibody which binds to a specific target
XX CC antigen. The antibody is esp. a single chain antibody in which the
XX CC heavy and light chain variable regions are joined via a hydrophilic
XX CC linker peptide. Localisation sequences are pref. included in the
XX CC constructs. The sequence AAR48260 is a mitochondrial matrix retention
XX CC signal.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ
XX Query Match 42.4%; Score 92; DB 15; Length 32;
XX Best Local Similarity 61.3%; Pred. No. 6.8e-07;
XX Matches 19; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 MLSNRLILNKAALRKAHTSMVRNFRYGRPV 31
DB 1 MLFNLRXXLNNAAFRHGHFMVNRFCGGQPL 31

RESULT 7
AAW96358
ID AAW96358 standard; Peptide; 32 AA.
XX AC AAW96358;
XX AC
XX DT 19-JUL-1999 (first entry)
XX DE Mitochondrial matrix localisation signal peptide.
XX KW Antibody; immune response; modulation; MHC; IRM; receptor;
XX KW intrabody; major histocompatibility complex; graft rejection;
XX KW immunomodulatory response molecule; regulation; transplantation;
XX KW retention signal; localisation signal; golgi apparatus; ER;

```

```

KW endoplasmic reticulum.
XX OS
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 7 /note= "Any amino acid"
XX FT Misc-difference 8 /note= "Any amino acid"
XX FT Misc-difference 32 /note= "Any amino acid"
XX FT
XX PN WO9914353-A2.
XX PD 25-MAR-1999.
XX PF 18-SEP-1998; 98WO-US19563.
XX PR 19-SEP-1997; 97US-0059339.
XX PA (DAND ) DANA FARBER CANCER INST INC.
XX PI Marasco W, Khashikar A;
XX XX WPI; 1999-229546/19.
XX PT Altering the regulation of the immune system
XX PS
XX PS Disclosure; Page 28; 56pp; English.
XX CC Intracellular binding to a desired target by an intracellularly
XX CC expressed antibody (i.e. an intrabody) can be used to knock out
XX CC multiple locuses of immunomodulatory receptor molecules (IRMs),
XX CC so that the expression of multiple major histocompatibility (MHC)
XX CC molecules is blocked. This selective targeting of IRMs, their
XX CC pathways or components, can be used to selectively regulate the
XX CC immune system by controlling expression of these molecules and
XX CC preventing an undesired immune response in a cell. Any component
XX CC of the MHC pathway or the MHC assembly line or antigen presentation
XX CC can be targeted. Intrabodies can be used to knock out the immune
XX CC response in a particular tissue or portion of the body to prepare
XX CC it for cell or tissue transplantation. Alternatively, an organ for
XX CC transplantation can be perfused with the intrabody ex vivo. The
XX CC intrabodies can comprise whole antibodies, heavy chains, Fab'
XX CC fragments, single-chain antibodies and diabodies. The intrabodies
XX CC also comprise an intracellular localisation signal to facilitate
XX CC interception of expressed proteins. For example, if the target was
XX CC a cell surface receptor, the antibody would comprise a leader
XX CC sequence and an endoplasmic reticulum (ER) or Golgi apparatus
XX CC retention signal. This peptide is a localisation sequence for the
XX CC mitochondrial matrix. For other localisation sequences see
XX CC AAW96345-W96377.
XX SQ
XX Query Match 42.4%; Score 92; DB 20; Length 32;
XX Best Local Similarity 61.3%; Pred. No. 6.8e-07;
XX Matches 19; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 MLSNRLILNKAALRKAHTSMVRNFRYGRPV 31
DB 1 MLFNLRXXLNNAAFRHGHFMVNRFCGGQPL 31

RESULT 8
ABG92993
ID ABG92993 standard; Peptide; 32 AA.
XX AC ABG92993;
XX AC
XX DT 20-NOV-2002 (first entry)
XX DE Localisation sequence to direct antibodies to the mitochondria.

```

XX Regulator; transcription; cell death; phenotype; molecular scaffold;
KW gene therapy; cancer; cardiovascular disease; arrhythmia; heart failure;
KW ischaemia; obesity; neurodegenerative disease; Alzheimer's disease;
KW bone pathology; dermatologic disease; psoriasis; infection; AIDS;
KW acquired immunodeficiency syndrome; cosmetic; wound healing;
KW antibiotic transport; drug toxicity; drug resistance; immunobiology;
KW inflammation; allergic response; human immunodeficiency virus.
XX Unidentified.
XX WO200262822-A2.
XX PD 15-AUG-2002.
XX PF 04-FEB-2002; 2002WO-US02814.
XX PR 02-FEB-2001; 2001US-265589P.
XX PR 05-FEB-2001; 2001US-265880P.
XX PR 27-FEB-2001; 2001US-271423P.
XX PR 23-JAN-2001; 2001US-263226P.
XX PR 28-MAR-2000; 2000US-192586P.
XX PR 22-SEP-1997; 97US-935377P.
XX PA (UYRP) UNIV ROCHESTER.
XX PI Zauderer M, Smith ES;
XX WPI; 2002-643398/69.
XX Identifying regulator polypeptides which influence target
PT transcriptional regulatory regions, useful for treating cancer,
PT comprises introducing host cells expressing the polypeptide into a
PT library of polynucleotides -
XX
PS Disclosure; Page 37; 224pp; English.
XX The invention discloses a method for identifying polynucleotides encoding
CC a regulator polypeptide, whose expression induces activation of a target
CC transcriptional regulatory region in a host cell. The method comprises
CC providing a population of eukaryotic host cells capable of expressing the
CC polypeptide, introducing into the host cell a library of polynucleotides
CC encoding the polypeptides, permitting expression of the polypeptides and
CC then recovering them from the host cells. The target transcriptional
CC regulatory region is operably associated with a polynucleotide encoding a
CC gene product, the expression of which results in host cell death or cause
CC the host cells to exhibit a pre-determined modified phenotype and where
CC the gene product is expressed upon activation of target transcriptional
CC regulatory region. Each candidate regulator polypeptide comprises a
CC candidate peptide and a molecular scaffold fused to the peptide so that
CC the peptide is displayed on the surface of the candidate regulator
CC polypeptide. The methods are useful in selecting and/or screening
CC regulator molecules, such as polypeptides, which directly or indirectly
CC induce or suppress the transcriptional activation of a target
CC transcriptional regulatory region in a eukaryotic host cell. These
CC regulator molecules may be used (e.g. in gene therapy) for preventing or
CC treating cancers (e.g. breast or ovarian cancer), cardiovascular diseases
CC (e.g. arrhythmia, heart failure, ischaemia), obesity, neurodegenerative
CC diseases (e.g. Alzheimer's disease), bone pathologies, dermatologic
CC diseases (e.g. psoriasis), infections (e.g. viral, bacterial), acquired
CC immunodeficiency syndrome (AIDS), in cosmetic applications and in wound
CC healing. The method is also useful in screening regulator molecules that
CC block antibiotic transport mechanisms, in drug toxicities and drug
CC resistance applications and in improving the performance of existing or
CC developmental drugs. It may also be used in immunobiology, inflammation,
CC allergic response and in biotechnology applications. The sequences
CC presented in ABG92946-ABG93029 are examples of regulator polypeptides.
XX Sequence 32 AA;
SQ Query Match 42.4%; Score 92; DB 23; Length 32;
Best Local Similarity 61.3%; Pred. No. 6.8e-07;
Matches 19; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 1 MSLNRLILLNKAALRKAFTSMVRNFRYKPV 31
||| ||| ||| ||| ||| ||| ||| |||
DB 1 MLENLRLXXLNNAAPRHGHENFVRNFRGQPL 31
RESULT 9
ABP56588
ID ABP56588 standard; Peptide; 32 AA.
XX AC ABP56588;
XX 24-MAR-2003 (first entry)
XX DE Mitochondrial matrix targeting peptide SEQ ID NO:54.
XX KW Identification; intrabody; eukaryotic cell; immunoglobulin; selection;
KW cardiovascular; diminished arrhythmia potential; cardiomyocyte; stroke;
KW enhanced contractile property; heart failure; arrhythmia; embolic;
KW sarcolemmal calcium cycling; artery; arteriole; angina; atherosclerosis;
KW LDL metabolism; HDL metabolism; skin biology; keloid formation.
XX OS Unidentified.
XX Key Location/Qualifiers
FH Misc-difference 7 /note= "any amino acid"
FT Misc-difference 8 /note= "any amino acid"
FT Misc-difference 32 /note= "any amino acid"
FT Misc-difference 32 /note= "any amino acid"
XX WO200286096-A2.
XX PD 31-OCT-2002.
XX PF 23-JAN-2002; 2002WO-US01677.
XX PR 23-JAN-2001; 2001US-263225P.
XX PR 24-JAN-2001; 2001US-263200P.
XX PR 27-FEB-2001; 2001US-271422P.
XX PR 15-JUN-2001; 2001US-298095P.
XX PA (UYRP) UNIV ROCHESTER MEDICAL CENT.
XX Zauderer M, Wei C, Smith ES;
XX WPI; 2003-103408/09.
XX Selecting polynucleotides encoding an intracellular immunoglobulin
PT which induces a modified phenotype in a eukaryotic host cell, by
PT introducing library of polynucleotides encoding immunoglobulin subunit
PT polypeptides -
XX Disclosure; Page 44; 257pp; English.
XX The present invention describes a method for selecting polynucleotides
CC (PNS) encoding an intracellular immunoglobulin molecule or its fragment
CC whose expression induces a modified phenotype in a eukaryotic host cell
CC (I). The method comprises introducing into (I) a first and second library
CC of PNS encoding, through operable association with a transcriptional
CC control region, first and second intracellular immunoglobulin subunit
CC polypeptides, respectively. The method is useful for selecting
CC polynucleotides which encode an intracellular immunoglobulin molecule, or
CC fragment. The method is useful e.g. for identifying polynucleotides which
CC singly or collectively encode intracellular immunoglobulin molecules, or
CC which sensitize host cells to killing by an agent. The method may also be
CC used in cardiovascular applications; for screening for diminished
CC arrhythmia potential in cardiomyocytes and for enhanced contractile
CC properties of cardiomyocytes and diminish heart failure potential; for
CC identifying intracellular immunoglobulin molecules that will regulate
CC intracellular and sarcolemmal calcium cycling in cardiomyocytes to
CC prevent arrhythmias or that will diminish embolic phenomena in arteries

CC and arterioles leading to strokes and angina; in screening for decreases
 CC in atherosclerosis-producing mechanisms to find intracellular
 CC immunoglobulin molecules that regulate LDL and HDL metabolism; in skin
 CC biology applications; and in regulating or inhibiting keloid formation.
 CC AB22379 to AB22449 and ABP5636 to ABP56618 represent sequences used in
 CC the exemplification of the present invention.

XX Sequence 32 AA;

Query Match 42.4%; Score 92; DB 24; Length 32;
 Best Local Similarity 61.3%; Pred. No. 6.8e-07;
 Matches 19; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 MLSNRLILLNKAALRKAHTSMVRNFRYKPV 31
 ||||| - - - - - ||||| : : :
 Db 1 MLFNLRXLNNAAFRHGHFMVFRFCGQPL 31

RESULT 10

AAB15704

ID AAB15704 standard; Peptide; 31 AA.

XX AC AAB15704;

XX DT 08-JAN-2001 (first entry)

XX DE Mitochondrial matrix localisation sequence.

XX KW Mitochondrial matrix localisation sequence; single-chain antibody;

XX KW stabilising fusion peptide; vaccine; gene therapy;

XX KW protein degradation modulation; protein stability; Alzheimer's disease.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Misc-difference 7 /note= "unspecified amino acid"

FT Misc-difference 31 /note= "unspecified amino acid"

FT WO200042185-A1.

XX PD 20-JUL-2000.

XX PF 11-JAN-2000; 2000WO-US00558.

XX PR 11-JAN-1999; 99US-0115505.

XX PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.

XX PI (MCIN/) MCINNIS P A.

XX Chain DG;

XX WPI; 2000-476059/41.

XX Modulating degradability of protein or peptide useful for gene therapy

XX involving antibodies, comprises altering a gene at the N terminus to

XX render protein or peptide metabolically stable.

XX Disclosure; Page 50; 76pp; English.

XX The present sequence is a localisation sequence that can be used to

XX direct stabilised single-chain antibodies to the mitochondrial matrix.

XX The N-terminus of the single-chain antibody is linked to a stabilising

XX fusion peptide, referred to as a stabilon, which increases stability of

XX the antibody against proteolysis in vivo. Degradation of the antibody

XX may be modulated by linking the stabilon to the antibody through a

XX protease-sensitive linker region. The stabilon is removed upon induction

XX of expression of a specific restriction protease by means of an

XX inducible promoter, and this renders the antibody susceptible to

XX proteolysis by the N-end rule pathway. This method for regulating

XX protein stability allows removal of the antibody after it has bound to

XX its target antigen. Stabilised recombinant proteins may be used in gene

CC therapy for the treatment of disorders such as Alzheimer's disease.

XX Sequence 31 AA;

XX Query Match 36.6%; Score 79.5; DB 21; Length 31;

XX Best Local Similarity 61.3%; Pred. No. 5.8e-05;

XX Matches 19; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

QY 1 MLSNRLILLNKAALRKAHTSMVRNFRYKPV 31

||||| - - - - - ||||| : : :
 Db 1 MLFNLRXLNNAAFRHGHFMVFRFCGQPL 30

RESULT 11

AAB22835

ID AAB22835 standard; peptide; 31 AA.

XX AC AAB22835;

XX DT 10-JAN-2001 (first entry)

XX DE Mitochondrial matrix localisation signal.

XX KW Controlled release delivery system; drug targeting;

XX KW drug-specific antibody; intracellular half-life; gene therapy;

XX KW diabetes; autoimmune disease; inflammatory disease; infectious disease;

XX KW cancer; side effect; subcellular localisation sequence.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Misc-difference 7 /label= unknown

FT Misc-difference 31 /label= unknown

FT WO200050089-A2.

XX PD 31-AUG-2000.

XX PF 25-FEB-2000; 2000WO-US04749.

XX PR 26-FEB-1999; 99US-0122103.

XX PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.

XX Chain DG;

XX WPI; 2000-572044/53.

XX Delivering a drug, to a patient suffering from cancer or diabetes, at a

XX predetermined site, comprises altering a target cell to express a drug

XX specific antibody by gene therapy and administering the drug.

XX Disclosure; Page 44; 69pp; English.

XX The invention relates to a controlled release drug delivery system.

XX Target cells in a patient are transformed with an expression construct

XX encoding an antibody (particularly a single chain antibody) to the drug

XX to be delivered. The antibody contains a modulator of intracellular

XX half-life; this can either be a stabilising or destabilising residue

XX located in the N-terminus after the initial methionine, or a peptide

XX ("stabilon") containing a stabilising residue linked to the antibody

XX N-terminus via a protease cleavage site. On administration of the drug,

XX the antibody binds the drug, localising it at the target cells but

XX maintaining it in an inactive state. As the antibody is degraded (the

XX timescale for which is dependent upon the N-terminal or stabilon amino

XX acids), the drug is released at its site of action where it can exert

XX its effects. The antibody encoded by the expression construct (and

XX therefore the therapeutic agent) can be targeted to particular

XX subcellular locations (e.g., the nucleus) by including the appropriate

XX cellular localisation signals. The novel method may be used to deliver

XX therapeutic agents to patients with a variety of conditions such as

diabetes, autoimmune diseases, inflammatory diseases, infectious diseases and especially cancer. The delivery method of the invention causes a drug to become almost immediately localised at its site of action in an inactive form where it accumulates. Once released by antibody degradation, the drug is at an effective concentration only at the target site, with very little free drug being available in the rest of the body. The system of the invention therefore reduces the side effects caused by therapeutic agents, and also provides economic benefits as a smaller amount can be administered to the patient. Sequences AAB22833 - AAB22837 and AAB22839-822857 represent subcellular localisation sequences which can be incorporated into a drug-specific antibody used in the method of the invention.


```
ABE59259
ID  ABB59259 standard; Protein; 755 AA.
XX
AC  ABB59259;
XX
DT  26-MAR-2002 (first entry)
XX
DE  Drosophila melanogaster polypeptide SEQ ID NO 4569.
XX
KW  Drosophila; developmental biology; cell signalling; insecticide;
KW  Pharmaceutical.
XX
OS  Drosophila melanogaster.
XX
PN  WC200171042-A2.
XX
PD  27-SEP-2001.
XX
PF  23-MAR-2001; 2001WO-US09231.
XX
PR  23-MAR-2000; 2000US-191637P.
PR  11-JUL-2000; 2000US-0614150.
XX
PA  (PEKE ) PE CORP NY.
XX
PI  Venter JC, Adams M, Li PWD, Myers EW;
XX
WI  WPI; 2001-656860/75.
DR  N-PSDB; ABL03362.
XX
XX  New isolated nucleic acid detection reagent for detecting 1000 or more
PT  genes from Drosophila and for elucidating cell signalling and cell-cell
PT  interactions -
XX
PS  Disclosure; SEQ ID NO 4569; 21pp + Sequence Listing; English.
XX
CC  The invention relates to an isolated nucleic acid detection reagent
CC  capable of detecting 1000 or more genes from Drosophila. The invention is
CC  useful in developmental biology and in elucidating cell signalling and
CC  cell-cell interactions in higher eukaryotes for the development of
CC  insecticides, therapeutics and pharmaceutical drugs. The invention
CC  discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC  sequences (ABL01840-ABL16175) and the encoded proteins
CC  (ABB57737-ABB72072).
CC  The sequence data for this patent did not form part of the printed
CC  specification, but was obtained in electronic format directly from WIPO
CC  at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ  Sequence 755 AA;

Query Match      24.7%; Score 53.5; DB 22; Length 755;
Best Local Similarity 42.5%; Pred. No. 33;
Matches 17; Conservative 5; Mismatches 15; Indels 3; Gaps 2;

QY  2 LSNRLTLNKAALRKRAHTSMVNFNRYGKPVQSQVOLKPRD 41
   ||::||| | ||||| : : || : : ||||
DB  11 LSDLRRELF--VLRKAHFELDLHFLYGTG-QPEAEAKPRD 47

RESULT 15
AAY04933
ID  AAY04933 standard; Protein; 165 AA.
XX
AC  AAY04933;
XX
DT  06-JUL-1999 (first entry)
XX
DE  Mycobacterium species protein sequence 388.
XX
KW  Secreted protein; Mycobacterium; primer; PCR; amplification; probe;
KW  hybridisation; detection; vaccine; immunisation; infection.
XX
OS  Mycobacterium sp.

XX  WO9909186-A2.
XX  25-FEB-1999.
XX  14-AUG-1998; 98WO-FR01813.
XX  11-SEP-1997; 97FR-0011325.
XX  14-AUG-1997; 97FR-0010404.
XX  (INSP ) INST PASTEUR.
XX  Gicquel B, Lim EM, Pelicic V, Portnoi D, Goguet de la Salmoniere Y;
XX  Guigueno A;
XX  WPI; 1999-181045/15.
DR  N-PSDB; AAX34186.
XX
XX  Mycobacterial DNA vectors containing reporter constructs - for
PT  identifying coding or promoter sequences involved in
PT  infection-associated protein expression
XX
PS  Claim 32; Flg 38B; 309pp; French.
XX
XX  Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted
CC  proteins from various Mycobacterium species microorganisms. The
CC  encoding nucleotide sequences can be used as primers and probes for
CC  methods for detecting and identifying mycobacteria, especially belonging
CC  to the M. tuberculosis complex. The encoded proteins can be used in
CC  vaccines for immunisation against a bacterial or viral infection.
XX
SQ  Sequence 165 AA;

Query Match      24.0%; Score 52; DB 20; Length 165;
Best Local Similarity 37.1%; Pred. No. 8.9;
Matches 13; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY  6 RILNKAALRKRAHTSMVNFNRYGKPVQSQVOLKPR 40
   ||:| | |||: | | :| :| :| :|
DB  119 RVILCAHTRKANQSRARTLRPLRPL--RIALRPR 151

Search completed: July 24, 2003, 22:04:08
Job time : 38.881 secs
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